

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 03:09:31 ; Search time 886 Seconds
(without alignments)
11458.669 Million cell updates/sec

Title: US-10-086-623-5
Perfect score: 1934
Sequence: 1 ttgtacgaagatgagac.....atcgacgaatactggaacccg 1934

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1934	100.0	1934	3	Ad00737 Human pla
2	1934	100.0	2253	3	Ad00738 Human pla
3	1934	100.0	2253	3	Ad00738 Human pla
4	1913.6	98.9	4001	5	Ad00738 Human pla
5	1913.6	98.9	4001	5	Ad00738 Human pla
6	1913.2	98.9	3739	10	Ad00738 Human pla
7	1913.2	98.9	3808	12	Ad00738 Human pla
8	1911.6	98.8	3798	5	Ad00738 Human pla
9	1911.6	98.8	3798	5	Ad00738 Human pla
10	1903.6	98.4	3718	6	Ad00738 Human pla
11	1903.6	98.4	3736	6	Ad00738 Human pla
12	1902.8	98.4	3853	4	Ad00738 Human pla
13	1896.2	98.0	4153	12	Ad00738 Human pla
14	1896.2	98.0	4153	12	Ad00738 Human pla
15	1896.2	98.0	4153	12	Ad00738 Human pla
16	1518.8	78.5	1587	4	Ad00738 Human pla
17	1518.8	78.5	1587	6	Ad00738 Human pla
18	1518.8	78.5	1587	6	Ad00738 Human pla
19	1518.8	78.5	1587	10	Ad00738 Human pla
20	1517.2	78.4	1587	10	Ad00738 Human pla
21	1517.2	78.4	1587	10	Ad00738 Human pla

22	1517.2	78.4	1587	10	Ad00738 Human pla
23	1517.2	78.4	1587	10	Ad00738 Human pla
24	1517.2	78.4	1587	10	Ad00738 Human pla
25	1517.2	78.4	1587	10	Ad00738 Human pla
26	1517.2	78.4	1587	12	Ad00738 Human pla
27	1505.2	77.8	1586	10	Ad00738 Human pla
28	1501.4	77.6	1728	4	Ad00738 Human pla
29	1501.4	77.6	1828	4	Ad00738 Human pla
30	1501.4	77.6	1828	6	Ad00738 Human pla
31	1501.4	77.6	1828	6	Ad00738 Human pla
32	1501.4	77.6	1828	10	Ad00738 Human pla
33	1498.2	77.5	1828	12	Ad00738 Human pla
34	1491.8	77.1	1882	3	Ad00738 Human pla
35	1491.8	77.1	1882	3	Ad00738 Human pla
36	1491.8	77.1	1882	4	Ad00738 Human pla
37	1491.8	77.1	1882	6	Ad00738 Human pla
38	1491.8	77.1	1882	6	Ad00738 Human pla
39	1491.8	77.1	1882	6	Ad00738 Human pla
40	1491.8	77.1	1882	8	Ad00738 Human pla
41	1491.8	77.1	1882	8	Ad00738 Human pla
42	1491.8	77.1	1882	9	Ad00738 Human pla
43	1491.8	77.1	1882	10	Ad00738 Human pla
44	1491.8	77.1	1882	10	Ad00738 Human pla
45	1491.8	77.1	1882	10	Ad00738 Human pla

ALIGNMENTS

RESULT 1

AD00737
ID AD00737 standard; cDNA; 1934 BP.

AC AD00737;

DT 08-SEP-2000 (first entry)

DE Human Platelet Derived Growth Factor (PDGF)-D encoding partial cDNA #2.

KW VEGF-G; Vascular Endothelial Growth Factor; antithrombotic; tumour;

KW proliferative; activator; proliferation; differentiation; motility;

KW growth; PDGF-D receptor; antagonist; tissue remodelling; treat;

KW atherosclerosis; wound; metastasis; ss.

OS Homo sapiens.

EH Key Location/Qualifiers

FT CDS 1..969

FT FT /*tag= a

FT FT /partial

FT FT /product= "Human PDGF-D partial polypeptide #2"

FT FT /note= "5, truncated platelet derived growth factor"

WO2000027879-A1.

18-MAY-2000.

10-NOV-1999; 99WO-US026462.

10-NOV-1998; 98US-0107852P.

28-DEC-1998; 98US-0113937P.

26-AUG-1999; 99US-0150604P.

04-OCT-1999; 99US-0157108P.

05-OCT-1999; 99US-0157756P.

(LUDW-) LUDWIG INST CANCER RES.

(UYHE-) UNIV HELSINKI LICENSING LTD OY.

Eriksson U, Aase K, Ponten A, Lee X, Utela M, Alitalo K;

Oestman A, Heldin C;

WPI; 2000-376495/32.

DR P-PSDB; AAY71129.
XX Novel polynucleotides encoding a novel growth factor of cells expressing
PT a platelet-derived growth factor, useful for diagnostic and therapeutic
PT applications, e.g. concerning cancer.
XX
XX Claim 1; Fig 5; il1pp; English.
XX
XX The present sequence is the 5' truncated partial cDNA #2, encoding human
CC platelet derived growth factor (PDGF)-D, formally known as Vascular
CC Endothelial Growth Factor (VEGF)-G. It is derived from human foetal lung
CC lambda2.10 cDNA library. It belongs to the VEGF/PDGF family. It functions
CC as an activator of proliferation, differentiation, growth and motility of
CC cells, that express PDGF-D receptor. This sequence is useful for
CC inhibiting the growth of tumours, that express PDGF-D. Expression of PDGF
CC -D and its proteolytic cleavage for generating an activated truncated
CC form is useful for regulating receptor binding specificity of PDGF-D.
CC PDGF-D antagonist is useful for inhibiting tissue remodelling during the
CC invasion of tumour cells into normal cells. PDGF-D may be used to treat
CC wounds, atherosclerosis, metastasis and migration of smooth muscle cells
XX
XX Sequence 1934 BP; 632 A; 366 C; 394 G; 542 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 1934; DB 3; Length 1934;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1934; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGTCCGAGAGATGAGACCATCCAGGTGAAGGAAACGGCTACGTGAGAGTCTCTAGA 60
DB 1 TTGTCCGAGAGATGAGACCATCCAGGTGAAGGAAACGGCTACGTGAGAGTCTCTAGA 60
QY 61 TTCCGAGAGATGAGACCATCCAGGTGAAGGAAACGGCTACGTGAGAGTCTCTAGA 120
DB 61 TTCCGAGAGATGAGACCATCCAGGTGAAGGAAACGGCTACGTGAGAGTCTCTAGA 120
QY 121 ACACGATACAGTGTGTTGACATCAGTTGGATTAGAGAGAGCGAATAATGATATC 180
DB 121 ACACGATACAGTGTGTTGACATCAGTTGGATTAGAGAGAGCGAATAATGATATC 180
QY 181 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCAAGTACCATTTATAGAGA 240
DB 181 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCAAGTACCATTTATAGAGA 240
QY 241 CGATGGTGTGACACAAAGAAAGTTCTCCAGGATAAAATCAAGAACCAACAAATTTAA 300
DB 241 CGATGGTGTGACACAAAGAAAGTTCTCCAGGATAAAATCAAGAACCAACAAATTTAA 300
QY 301 ATCAGATTCAGTCCGATGACTACTTGTGGCTAAACCTGGATTCAAGATTATTTCT 360
DB 301 ATCAGATTCAGTCCGATGACTACTTGTGGCTAAACCTGGATTCAAGATTATTTCT 360
QY 361 TTGCTGGAAAGATTCCAAACCCAGCAGCTTCAGAGACCAACTGGGAATCTGTCAAGC 420
DB 361 TTGCTGGAAAGATTCCAAACCCAGCAGCTTCAGAGACCAACTGGGAATCTGTCAAGC 420
QY 421 TCTATTTCCAGGGATATCTTAACTCTCCATCAGTAAACCGATCCCACTCTGATTCGGAT 480
DB 421 TCTATTTCCAGGGATATCTTAACTCTCCATCAGTAAACCGATCCCACTCTGATTCGGAT 480
QY 481 GCTCTGGACAAAATAATTCAGAAATTTGATACAGTGGAGATCTGCTCAAGTACTTCAAT 540
DB 481 GCTCTGGACAAAATAATTCAGAAATTTGATACAGTGGAGATCTGCTCAAGTACTTCAAT 540
QY 541 CCAGAGTTCATGCAAGAGATCTTGAGAAATGATCTGGACACCCCTCGGTATCGAGC 600
DB 541 CCAGAGTTCATGCAAGAGATCTTGAGAAATGATCTGGACACCCCTCGGTATCGAGC 600
QY 601 AGGTATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
DB 601 AGGTATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
QY 661 CGTTACAGTTGACCTCCCAAGGAATTTACCTCGGTCAATATAAGAGAGAGCTCAAGTTGCC 720
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DB 661 CGTTACAGTTGACCTCCCAAGGAATTTACTCGGTCAATATAAGAGAGAGCTCAAGTTGCC 720
QY 721 AATGTGCTCTCTTTTCCAGCTTGCCTCTCTGTCAGCCTGTGAGAGAAATTTGGCTGT 780
DB 721 AATGTGCTCTCTTTTCCAGCTTGCCTCTCTGTCAGCCTGTGAGAGAAATTTGGCTGT 780
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DB 841 GAGGTATTACAGTTTGGAGCTGGCCACATCAAGAGAGGGGTAGAGCTTAAGACCATGCT 900
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QY 1021 GGGTGAATTAAGAGACCTTTTCTTACCAAGCAACCAACTTACTACTAGCCTGCAATGCA 1080
DB 1021 GGGTGAATTAAGAGACCTTTTCTTACCAAGCAACCAACTTACTACTAGCCTGCAATGCA 1080
QY 1081 ATGAACACAGTGTGCTGAGTCTCAGCCTTGTGTTTAAATAGTGTGTTGAG 1140
DB 1081 ATGAACACAGTGTGCTGAGTCTCAGCCTTGTGTTTAAATAGTGTGTTGAG 1140
QY 1141 GGTATATCATCAACTTCTATACCTAAGATATAGATTTGATTTAAATAGTGTGTTGAG 1200
DB 1141 GGTATATCATCAACTTCTATACCTAAGATATAGATTTGATTTAAATAGTGTGTTGAG 1200
QY 1201 GTTATATATGACAAACACACACAGAAATATATTCATGTCTATGTATATAGATCAAT 1260
DB 1201 GTTATATATGACAAACACACACAGAAATATATTCATGTCTATGTATATAGATCAAT 1260
QY 1261 GTTTTTTTTGGTATATATTAACAGGTACACAGAGCTTACATATGTTGAGTTAGCTCT 1320
DB 1261 GTTTTTTTTGGTATATATTAACAGGTACACAGAGCTTACATATGTTGAGTTAGCTCT 1320
QY 1321 TAAATCCTTTGCCAAATAGGATGCTCAAAATATATGAACATGCTTTTGAAGAAATTT 1380
DB 1321 TAAATCCTTTGCCAAATAGGATGCTCAAAATATATGAACATGCTTTTGAAGAAATTT 1380
QY 1381 AGGATATAATTTATTTTAAATTTTGAACACAAATTTTGAATCTTGTCTCTCTTA 1440
DB 1381 AGGATATAATTTATTTTAAATTTTGAACACAAATTTTGAATCTTGTCTCTCTTA 1440
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DB 1441 AAGAAAGCATCTTGTATATTAATAATCAAGAGATGAGCTTCTTACATATACATCTTAG 1500
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DB 1501 TTGATTTATTAAGAAAGAAAGGTTTCCAGAGAAAGGCAATACCTAAGCATTTTTTC 1560
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DB 1561 CATGAGAGCATCTGATCTTACCTATGTGAGCTGTAATTAACCTGTCTCAAAACCAATGC 1620
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DB 1621 CATATAATATAAGTGTCTTGAAGAAATTAATCATTTGTTTTTATGCAATTTGCTGAGG 1680
QY 1681 CATCTTATTTCAATTAACCTATCTCAAAACCTTACTTAGAAGGTTTTTATTTATATAGTC 1740
DB 1681 CATCTTATTTCAATTAACCTATCTCAAAACCTTACTTAGAAGGTTTTTATTTATATAGTC 1740
QY 1741 CTACAAAGACATGATATAGCTGTACAGAAATTTGAAATTTTCTTTTTCGAAACCC 1800
DB 1741 CTACAAAGACATGATATAGCTGTACAGAAATTTGAAATTTTCTTTTTCGAAACCC 1800

Qy 1801 CTCACAAAAGCAAAATCTTTCAAGAATGGCATGGGCAATCTGTATGAACCTTTCCAGAT 1860
 Db 1801 CTCACAAAAGCAAAATCTTTCAAGAATGGCATGGGCAATCTGTATGAACCTTTCCAGAT 1860
 Qy 1861 GGTGTTTCAGTGAAGAGTGGTGTAGTTGAGNACTTAAAGAGTGAACATTTGAAACATCGAC 1920
 Db 1861 GGTGTTTCAGTGAAGAGTGGTGTAGTTGAGNACTTAAAGAGTGAACATTTGAAACATCGAC 1920
 Qy 1921 GTAACCTGGAACCG 1934
 Db 1921 GTAACCTGGAACCG 1934
 RESULT 2
 AAD00738
 ID AAD00738 standard; cDNA; 2253 BP.
 XX
 AC AAD00738;
 XX
 DT 08-SEP-2000 (first entry)
 XX
 DE Human Platelet Derived Growth Factor (PDGF)-D encoding complete cDNA.
 KW Platelet Derived Growth Factor-D; PDGF-D; human; cytostatic; vulnery;
 KW VEGF-G; Vascular Endothelial Growth Factor; antiatherosclerotic; tumour;
 KW proliferative; activator; proliferation; differentiation; motility;
 KW growth; PDGF-D receptor; antagonist; tissue remodelling; treat;
 KW atherosclerosis; wound; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 176..1288
 FT /*tag= a
 FT /product= "Human PDGF-D protein"
 FT /note= "Platelet derived growth factor"
 XX
 PN W0200027879-A1.
 XX
 PD 18-MAY-2000.
 XX
 PF 10-NOV-1999; 99WO-US026462.
 XX
 PR 10-NOV-1998; 98US-0107852P.
 PR 28-DEC-1998; 98US-0113997P.
 PR 26-AUG-1999; 99US-0150604P.
 PR 04-OCT-1999; 99US-0157108P.
 PR 05-OCT-1999; 99US-0157756P.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
 XX
 PI Eriksson U, Aase K, Ponten A, Lee X, Uutela M, Alitalo K;
 PI Oestman A, Heldin C;
 XX
 DR WPI: 2000-376495/32.
 DR P-PSDB: AAY71130.
 XX
 FT Novel polynucleotides encoding a novel growth factor of cells expressing
 FT a platelet-derived growth factor, useful for diagnostic and therapeutic
 FT applications, e.g. concerning cancer.
 XX
 PS Claim 1; Fig 7; 111pp; English.
 XX
 CC The present sequence is the complete cDNA encoding human platelet derived
 CC growth factor (PDGF)-D, formally known as Vascular Endothelial Growth
 CC Factor (VEGF)-G. It is derived from human foetal lung lambda gt10 cDNA
 CC library. It belongs to the VEGF/PDGF family. It functions as an activator
 CC of proliferation, differentiation, growth and motility of cells, that
 CC express PDGF-D receptor. This sequence is useful for inhibiting the
 CC growth of tumours, that express PDGF-D. Expression of PDGF-D and its
 CC proteolytic cleavage for generating an activated truncated form is useful

CC for regulating receptor binding specificity of PDGF-D. PDGF-D antagonist
 CC is useful for inhibiting tissue remodelling during the invasion of tumour
 CC cells into normal cells. PDGF-D may be used to treat wounds,
 CC atherosclerosis, metastasis and migration of smooth muscle cells
 XX
 SQ Sequence 2253 BP; 701 A; 464 C; 490 G; 598 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1934; DB 3; Length 2253;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1934; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAGGAAACGGCTACGTGCGAGGTCCTAGA 60
 Db 320 TTGTACCGAAGAGATGAGACCATCCAGGTGAAGGAAACGGCTACGTGCGAGGTCCTAGA 379
 Qy 61 TTCCCGAAACAGCTACCCCGAGAACCTCTCTCTGACATGGGGCTTCACTCTCAGGAGAAT 120
 Db 380 TTCCCGAAACAGCTACCCCGAGAACCTCTCTCTGACATGGGGCTTCACTCTCAGGAGAAT 439
 Qy 121 ACACGGATACAGCTAGTGTGTTTGACAAATCAGTTTGGATTAGAGGAAGCAGAAAATGATATC 180
 Db 440 ACACGGATACAGCTAGTGTGTTTGACAAATCAGTTTGGATTAGAGGAAGCAGAAAATGATATC 499
 Qy 181 TGTAGGTATGATTTTGTGGAAGTTGAGATATATCCGAAACAGTACCATTATTAGAGGA 240
 Db 500 TGTAGGTATGATTTTGTGGAAGTTGAGATATATCCGAAACAGTACCATTATTAGAGGA 559
 Qy 241 CGATGGTGTGGACACAAGAGGAGTTCTTCCAAAGGATAAAATCAAGAACGAAACCAATTTAA 300
 Db 560 CGATGGTGTGGACACAAGAGGAGTTCTTCCAAAGGATAAAATCAAGAACGAAACCAATTTAA 619
 Qy 301 ATCAATTTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTATTATCT 360
 Db 620 ATCAATTTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTATTATCT 679
 Qy 361 TTGCTGAAGATTTCCAAACCGGAGAGCTTCAGAGACCAACTGGGATCTGTCAACAGC 420
 Db 680 TTGCTGAAGATTTCCAAACCGGAGAGCTTCAGAGACCAACTGGGATCTGTCAACAGC 739
 Qy 421 TCTATTTTCAGGGGTATCTTAACTCTCCATCAGTAAACGGATCCACTCTGATTCGGAT 480
 Db 740 TCTATTTTCAGGGGTATCTTAACTCTCCATCAGTAAACGGATCCACTCTGATTCGGAT 799
 Qy 481 GCTCTGGACAAAAAATTCAGAAATTTGATACAGTGAAGATCTGCTCAAGTACTTCAAT 540
 Db 800 GCTCTGGACAAAAAATTCAGAAATTTGATACAGTGAAGATCTGCTCAAGTACTTCAAT 859
 Qy 541 CCAGATCATGGCAAGAAAGATCTTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGC 600
 Db 860 CCAGATCATGGCAAGAAAGATCTTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGC 919
 Qy 601 AGGTCAATACATGACCGGAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
 Db 920 AGGTCAATACATGACCGGAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 979
 Qy 661 CGTTACAGTTGCACTCCCGAGGAATTTACTCGGTCAATATAAGAGAGAGCTGAAGTTGCC 720
 Db 980 CGTTACAGTTGCACTCCCGAGGAATTTACTCGGTCAATATAAGAGAGAGCTGAAGTTGCC 1039
 Qy 721 AATGTGTTCTTTTTCACAGTTGCTCTCTGTGAGCGCTGTGGAGGAAATTTGGCTGT 780
 Db 1040 AATGTGTTCTTTTTCACAGTTGCTCTCTGTGAGCGCTGTGGAGGAAATTTGGCTGT 1099
 Qy 781 GGAACCTCACTGGAGTCTCTGACATGCAATTTAGGGAACCGTCAAAAGATATCAT 840
 Db 1100 GGAACCTCACTGGAGTCTCTGACATGCAATTTAGGGAACCGTCAAAAGATATCAT 1159
 Qy 841 GAGGTATTACAGTTTGAAGCTTGGCCACATCAAGAGAGGGGTAGAGCTAAGACCAATGGCT 900
 Db 1160 GAGGTATTACAGTTTGAAGCTTGGCCACATCAAGAGAGGGGTAGAGCTAAGACCAATGGCT 1219
 Qy 901 CTAGTTGACATCCAGTTGGATTCACATGAACGATGCGGATTGTATCTGAGCTCAAGACCA 960

Db 1220 CTAGTTGACATCCAGTTGGATCACCATGAACGATCGGATTGTATCTGCAGCTCAAGACCA 1279
QY 961 CCTCGATAAGAGAAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTAAGGA 1020
Db 1280 CCTCGATAAGAGAAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTAAGGA 1339
QY 1021 GGGTGAGATAAGAGACCCCTTTTCTACACGACCAACAACTTACTACTAGCCTGCAATGCA 1080
Db 1340 GGGTGAGATAAGAGACCCCTTTTCTACACGACCAACAACTTACTACTAGCCTGCAATGCA 1399
QY 1081 ATGAACACAAAGTGTGTGCTGAGTCTCAGCCTTGTCTTGTAAATGCGATGCGCAAGTAGAAA 1140
Db 1400 ATGAACACAAAGTGTGTGCTGAGTCTCAGCCTTGTCTTGTAAATGCGATGCGCAAGTAGAAA 1459
QY 1141 GGTATATCATCAACTTCTATACCTAAGAAATATAGGATGCAATTAATAATAGTGTTCGAG 1200
Db 1460 GGTATATCATCAACTTCTATACCTAAGAAATATAGGATGCAATTAATAATAGTGTTCGAG 1519
QY 1201 GTTATATATGCAAAACACACACAGAAATATATGCTATGCTATGCTATATAGATCAAAAT 1260
Db 1520 GTTATATATGCAAAACACACACAGAAATATATGCTATGCTATGCTATATAGATCAAAAT 1579
QY 1261 GTTTTGTGTTGTTATATATAACAGGTACACAGAGCTTACATATCTTTGAGTTAGACTCT 1320
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QY 1321 TAAAAATCCTTTGCCAAAATAAGGGATGGTCAAAATATATGAAACATGCTCTTTAGAAAAATTT 1380
Db 1640 TAAATCCTTTGCCAAAATAAGGGATGGTCAAAATATATGAAACATGCTCTTTAGAAAAATTT 1699
QY 1381 AGGAGATAAATTTATTTTAAATTTTGAACACAAACAAATTTTGAATCTGCTCTCTTA 1440
Db 1700 AGGAGATAAATTTATTTTAAATTTTGAACACAAACAAATTTTGAATCTGCTCTCTTA 1759
QY 1441 PAGAAGATCTGTGTATATTAATAATCAAAACATGAGGCTTTCTTACATATACATCTTAG 1500
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QY 1501 TTGATTATTTAAAAAGGAAAAAGTTTCCAGAGAAAAAGGCCAATACCTAAGCAATTTTTC 1560
Db 1820 TTGATTATTTAAAAAGGAAAAAGTTTCCAGAGAAAAAGGCCAATACCTAAGCAATTTTTC 1879
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Db 1880 CATGAGAGCACTGCATCTTACCTATGTGGACTGTATTAACCTGTCTCTCAAAACCATGTC 1939
QY 1621 CATATAATATAAGTGTCTTTAGAAATTAATAATCAATTTGTTTATGCAATTTTGTGAGG 1680
Db 1940 CATATAATATAAGTGTCTTTAGAAATTAATAATCAATTTGTTTATGCAATTTTGTGAGG 1999
QY 1681 CATCTTATTTCAATTAACACCTATCTCAAAAACCTTACTTAGAAGGTTTTTTTATTATAGTC 1740
Db 2000 CATCTTATTTCAATTAACACCTATCTCAAAAACCTTACTTAGAAGGTTTTTTTATTATAGTC 2059
QY 1741 CTACAAAAGCAATGTATAAGCTGTAAACAGAAATTTTGAATGTTTCTTTGCAAAACCC 1800
Db 2060 CTACAAAAGCAATGTATAAGCTGTAAACAGAAATTTTGAATGTTTCTTTGCAAAACCC 2119
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Db 2120 CTCCACAAAGCAATCTTTCAAGATGGCATGGCAATTCGTATGACCTTTTCCAGAT 2179
QY 1861 GGTGTTTCAGTGAAGATGTGGGTAGTTGAGAACTTTAAAAAGTGAACATTTGAAACATCGAC 1920
Db 2180 GGTGTTTCAGTGAAGATGTGGGTAGTTGAGAACTTTAAAAAGTGAACATTTGAAACATCGAC 2239
QY 1921 GTAACCTGGAACCG 1934
Db 2240 GTAACCTGGAACCG 2253

ID XX ABQ80246 standard; cDNA; 2253 BP.
XX AC ABQ80246;
XX DT 27-JUN-2003 (first entry)
XX DE PDGF-D cDNA.
XX KW Gens; nervous system; platelet-derived growth factor; PDGF; psychosis;
KW vascular endothelial growth factor; VEGF; neural; stem cell; memory;
KW progenitor cell; neurodegeneration; ischaemia; neurological trauma;
KW neuropsychiatry; learning; Parkinson's disease; Huntington's disease;
KW Amyotrophic lateral Sclerosis; spinal ischaemia; ischaemic stroke;
KW spinal cord injury; cancer-related; schizophrenia; Alzheimer's disease;
KW depression; anxiety; phobia; stress; cognitive function; aggression;
KW drug; alcohol; abuse; obsessive compulsive behaviour; proliferation;
KW seasonal mood disorder; personality disorder; cerebral palsy;
KW multi-infarct; dementia; Lewy body; age related; geriatric; growth;
KW epilepsy; brain injury; multiple sclerosis; autism; differentiation;
KW attention deficit disorder; narcolepsy; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT CDS 176..1288
FT /*tag= a
FT /product= "PDGF-D"
XX WO2003024478-A1.
XX PD 27-MAR-2003.
XX PF 19-SEP-2002; 2002WO-IB003998.
XX PR 19-SEP-2001; 2001US-0323381P.
XX PR 28-SEP-2001; 2001US-0326044P.
XX XX
XX PA (NEUR-) NEURONOVA AB.
XX PI Delfani K, Janson AM, Kuhn GH, Plate K, Schanzer A, Wachs F;
PI Zhao M;
XX WPI; 2003-354563/33.
XX P-PSDB; ABB80134.
XX Use of platelet-derived growth factor, vascular endothelial growth
XX factor, or their modulators for modulating neural stem cell or neural
XX progenitor cell activity, particularly for treating e.g. Alzheimer's,
XX ischemia or stroke.
XX Claim 97; Page 22-23; 119pp; English.
XX The sequences given in ABQ80243-47 encode proteins which may be used in
XX the method of the invention for alleviating or reducing a symptom of a
XX disease or disorder of the nervous system. The method comprises
XX administering platelet-derived growth factor (PDGF), vascular endothelial
XX growth factor (VEGF), a combination of PDGF and VEGF, or a PDGF or VEGF
XX agonist, to a patient in order to modulate neural stem cell or neural
XX progenitor cell activity in vivo. The method is useful for alleviating or
XX reducing the symptoms of a disease or disorder of the nervous system,
XX e.g. neurodegenerative disorders, neural stem cell disorders, neural
XX progenitor disorders, ischaemic disorders, neurological traumas,
XX affective disorders, neuropsychiatric disorders or learning and memory
XX disorders. In particular, the method is useful for alleviating or
XX treating Parkinson's disease and disorders, Huntington's disease,
XX Alzheimer's disease, Amyotrophic Lateral Sclerosis, spinal ischaemia,
XX ischaemic stroke, spinal cord injury or cancer-related brain/ spinal cord
XX injury, schizophrenia and other psychoses, depression, bipolar
XX depression/disorder, anxiety syndromes/disorders, phobias, stress and
XX related syndromes, cognitive function disorders, aggression, drug and
XX alcohol abuse, obsessive compulsive behaviour syndromes, seasonal mood
XX disorder, borderline personality disorder, cerebral palsy, life style
XX drug, multi-infarct dementia, Lewy body dementia, age related/geriatric

CC dementia, epilepsy and injury related to epilepsy, spinal cord injury,
CC brain injury, trauma related brain/spinal cord injury, anti-cancer
CC treatment related brain/spinal cord tissue injury, infection and
CC inflammation related brain/spinal cord injury, environmental toxin
CC related brain/spinal cord injury, multiple sclerosis, autism, attention
CC deficit disorders, narcolepsy or sleep disorders. The PDGF and/or VEGF,
CC is useful in the manufacture of a medicament for alleviating or treating
CC these diseases or disorders, accelerating growth of neural stem cells or
CC neural progenitor cells, or inducing proliferation or differentiation of
CC these cells
XX
SQ Sequence 2253 BP; 701 A; 464 C; 490 G; 598 T; 0 U; 0 Other;

Query Match 100.0%; Score 1934; DB 8; Length 2253;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1934; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGTACCGAAGAGATGAGACATCCAGGTGAAGGAACCGCTACGTGCAGAGTCCTAGA 60
Db 320 TTGTACCGAAGAGATGAGACATCCAGGTGAAGGAACCGCTACGTGCAGAGTCCTAGA 379

Qy 61 TTCCGGAACAGCTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGAGAAAT 120
Db 380 TTCCGGAACAGCTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGAGAAAT 439

Qy 121 ACACGGATACAGCTAGTGTGTTGACAAATCAGTTGGATTAGAGGAAGCAAGAAATGATATC 180
Db 440 ACACGGATACAGCTAGTGTGTTGACAAATCAGTTGGATTAGAGGAAGCAAGAAATGATATC 499

Qy 181 TGTAGGTATGATTTGTGGAGTTGAAGATATATCCGAAACCCAGTACCATTATTAGAGGA 240
Db 500 TGTAGGTATGATTTGTGGAGTTGAAGATATATCCGAAACCCAGTACCATTATTAGAGGA 559

Qy 241 CGATGGTGTGACACAAAGGAAGTTCTCCAGAGTAAATCAAGAACCAACCAATTTAA 300
Db 560 CGATGGTGTGACACAAAGGAAGTTCTCCAGAGTAAATCAAGAACCAACCAATTTAA 619

Qy 301 ATCACTTTCAAGTCGGATGACTTTTGTGGCTAAACCTGGATTCAAGATTTATTATCT 360
Db 620 ATCACTTTCAAGTCGGATGACTTTTGTGGCTAAACCTGGATTCAAGATTTATTATCT 679

Qy 361 TTGCTGGAAGATTTCCACCCGACAGCTTCAGAGCAACCTGGGAATCTGTCAACGC 420
Db 680 TTGCTGGAAGATTTCCACCCGACAGCTTCAGAGCAACCTGGGAATCTGTCAACGC 739

Qy 421 TCTATTTTCAGGGGTATCCTATAACTCTCCATCAGTAAACGGATCCCACTCTGATTGCGGAT 480
Db 740 TCTATTTTCAGGGGTATCCTATAACTCTCCATCAGTAAACGGATCCCACTCTGATTGCGGAT 799

Qy 481 GCTCTGGAACAAAAATTCAGAAATTTGATACAGTGGGAAGATCTGCTCAAGTACTTCAAT 540
Db 800 GCTCTGGAACAAAAATTCAGAAATTTGATACAGTGGGAAGATCTGCTCAAGTACTTCAAT 859

Qy 541 CCAGAGTCATGGCAAGAGATCTTGAGATATGATATCTGACACCCCTCGGTATCGAGGC 600
Db 860 CCAGAGTCATGGCAAGAGATCTTGAGATATGATATCTGACACCCCTCGGTATCGAGGC 919

Qy 601 AGGTCAATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
Db 920 AGGTCAATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 979

Qy 661 CGTTACAGTTGACCTCCAGGAATTTACTCGGTCAATATAAGAGAAAGAGCTGAAGTTGCC 720
Db 980 CGTTACAGTTGACCTCCAGGAATTTACTCGGTCAATATAAGAGAAAGAGCTGAAGTTGCC 1039

Qy 721 AATGTGGTCTTTTTCAGAGTTGGCTCTCTGTCGAGCGCTGTGGAGGAAATTTGGGCTGT 780
Db 1040 AATGTGGTCTTTTTCAGAGTTGGCTCTCTGTCGAGCGCTGTGGAGGAAATTTGGGCTGT 1099

Qy 781 GGAATCTCACTGAGGAGTCTGACATGCAATTCAGGGAAACCGTGAAAGATATCAT 840
Db 1100 GGAATCTCACTGAGGAGTCTGACATGCAATTCAGGGAAACCGTGAAAGATATCAT 1159

Qy 841 GAGTATTACAGTTTGGCCCTGGCCACATCAAGAGGAGGGGTAGAGCTTAAGACCATGGCT 900
Db 1160 GAGTATTACAGTTTGGCCCTGGCCACATCAAGAGGAGGGGTAGAGCTTAAGACCATGGCT 1219

Qy 901 CTAGTTGACATCCAGTTGGATCAGATGAGAGTTCGATCTGTCAGCTCAAGACCA 960
Db 1220 CTAGTTGACATCCAGTTGGATCAGATGAGAGTTCGATCTGTCAGCTCAAGACCA 1279

Qy 961 CCTCGATAAGAGAAATGTCACATCCTTACATTAAGACCTGAAAGAACCTTTAGTTAAGGA 1020
Db 1280 CCTCGATAAGAGAAATGTCACATCCTTACATTAAGACCTGAAAGAACCTTTAGTTAAGGA 1339

Qy 1021 GGGTGAGATAAGAGACCCCTTTTCTACCAAGCAACCAACTTACTACTAGCTGCAATGCA 1080
Db 1340 GGGTGAGATAAGAGACCCCTTTTCTACCAAGCAACCAACTTACTACTAGCTGCAATGCA 1399

Qy 1081 ATGAACAACAGTGGTGTCTGAGTCTCAGCCCTTGTCTTGTAAATGCGCATGGCAAGTAGAAA 1140
Db 1400 ATGAACAACAGTGGTGTCTGAGTCTCAGCCCTTGTCTTGTAAATGCGCATGGCAAGTAGAAA 1459

Qy 1141 GGTATATCATCAACTTCTATACCTTAAGAAATATAGGATTTGCAATTTAATAATAGTGTTCAG 1200
Db 1460 GGTATATCATCAACTTCTATACCTTAAGAAATATAGGATTTGCAATTTAATAATAGTGTTCAG 1519

Qy 1201 GTTATATATGACACAAACACACACACAGAAATATATTCTGTCCTATGTTATATAGATCAAT 1260
Db 1520 GTTATATATGACACAAACACACACAGAAATATATTCTGTCCTATGTTATATAGATCAAT 1579

Qy 1261 GTTTTTTTTGGTATATATAACCCAGGTACACAGAGCTTACATATGTTTGGATTAGACTCT 1320
Db 1580 GTTTTTTTTGGTATATATAACCCAGGTACACAGAGCTTACATATGTTTGGATTAGACTCT 1639

Qy 1321 TAAATCCTTTTGGCCAAATAAAGGATGCTCAAAATATATGAAACCATGCTTTTAGAAAAATTT 1380
Db 1640 TAAATCCTTTTGGCCAAATAAAGGATGCTCAAAATATATGAAACCATGCTTTTAGAAAAATTT 1699

Qy 1381 AGGAGATAAATTTATTTTAAATTTTGAACACAAAACAATTTTGAATCTTGCTCTCTTA 1440
Db 1700 AGGAGATAAATTTATTTTAAATTTTGAACACAAAACAATTTTGAATCTTGCTCTCTTA 1759

Qy 1441 AAGAAAGCATCTCTGTATATAAATAAAGAGATGAGGCTTTCTTACATATACATCTTAG 1500
Db 1760 AAGAAAGCATCTCTGTATATAAATAAAGAGATGAGGCTTTCTTACATATACATCTTAG 1819

Qy 1501 TTGATTATTAATAAAGGAAAAAGGTTTCCAGAGAAAAAGGCAATACTTAAGCATTTTTC 1560
Db 1820 TTGATTATTAATAAAGGAAAAAGGTTTCCAGAGAAAAAGGCAATACTTAAGCATTTTTC 1879

Qy 1561 CATGAGAAGCACTGCATCTTACCTATGTGACTGTATAACCTGTCTCCAAAAACCATGC 1620
Db 1880 CATGAGAAGCACTGCATCTTACCTATGTGACTGTATAACCTGTCTCCAAAAACCATGC 1939

Qy 1621 CATATAATATAAGTGTCTTTAGAAAAATTAATCATTTGTTTTTATGCAATTTTGTGAGG 1680
Db 1940 CATATAATATAAGTGTCTTTAGAAAAATTAATCATTTGTTTTTATGCAATTTTGTGAGG 1999

Qy 1681 CATCCTTATTCATTAAACACCTATCTCAAAAACTTACTTTAGAGAGGTTTTTTATTATAGTC 1740
Db 2000 CATCCTTATTCATTAAACACCTATCTCAAAAACTTACTTTAGAGAGGTTTTTTATTATAGTC 2059

Qy 1741 CTACAAAAAGCAATGTATAGCTGTAAAGAAATTTGAAATTTGTTTTTCTTTGCAAAACCC 1800
Db 2060 CTACAAAAAGCAATGTATAGCTGTAAAGAAATTTGAAATTTGTTTTTCTTTGCAAAACCC 2119

Qy 1801 CTCACAAAAAGCAATCCTTTTCAAGAAATGGCATGGCATTTCTGTATGAACCTTTCCAGAT 1860
Db 2120 CTCACAAAAAGCAATCCTTTTCAAGAAATGGCATGGCATTTCTGTATGAACCTTTCCAGAT 2179

Qy 1861 GGTGTTTCAGTGAAGAGATGGGTAGTTGAGAACTTTAAAAAGTGAAACATTTGAAACATCGAC 1920
Db 2180 GGTGTTTCAGTGAAGAGATGGGTAGTTGAGAACTTTAAAAAGTGAAACATTTGAAACATCGAC 2239

Qy 1921 GTAACTGGAACCCG 1934

Db 2240 GTAACCTGGAACCG 2253
 RESULT 4
 AAH46957
 ID AAH46957 standard; cDNA; 4001 BP.
 XX
 AC AAH46957;
 DT 25-SEP-2001 (first entry)
 XX
 DE Human secreted protein encoding cDNA (clone Id HBTV90).
 XX
 KW Secreted protein; immunosuppressive; antiarthritic; antirheumatic;
 KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
 KW neotropic; neuroprotective; antibacterial; virucide; fungicide; human;
 KW ophthalmological; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200155430-A1.
 XX
 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US0001431.
 XX
 PR 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 12-SEP-2000; 2000US-0231968P.
 XX
 PR (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX
 PI Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR;
 PI Olsen HS, Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH;
 PI Fiscella M, Ni J, Ruben SM, Barash SC;
 XX
 DR WPI; 2001-476220/S1.
 DR F-PSDB; AAB85547.
 XX
 PT 17 isolated nucleic acid molecules encoding human secreted proteins, used
 to preventing, treating or ameliorating a medical condition.
 XX
 PS Claim 1; Page 430-432; 482pp; English.
 XX
 CC The invention provides novel human secreted proteins and polynucleotides
 CC encoding them. The secreted proteins can be expressed by standard
 CC recombinant methodology. The secreted proteins and polynucleotides are
 CC used to prevent, treat or ameliorate a medical condition in e.g. humans,
 CC mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They can
 CC also be used in diagnosing a pathological condition. The antibodies to
 CC the proteins can also be used in alleviating symptoms associated with the
 CC disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme
 CC linked immunosorbent assays (ELISA). Disorders which are diagnosed or
 CC treated include autoimmune diseases e.g. rheumatoid arthritis,
 CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
 CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
 CC e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g.
 CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and
 CC ocular disorders e.g. corneal infection. The polypeptides can also be
 CC used to aid wound healing and epithelial cell proliferation, to prevent
 CC skin aging due to sunburn, to maintain organs before transplantation, for
 CC supporting cell culture of primary tissues, to regenerate tissues and in
 CC chemotaxis. The polypeptides can also be used as a food additive or
 CC preservative to increase or decrease storage capabilities. The present
 CC sequence represents a human secreted protein encoding cDNA
 XX
 SQ Sequence 4001 BP; 1218 A; 823 C; 796 G; 1156 T; 0 U; 8 Other;
 Query Match 98.9%; Score 1913.6; DB 5; Length 4001;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 1923; Conservative 1; Indels 3; Gaps 1;

QY 1 TTGTACCGAAGAGATGAGACCAATCCAGGTGAAAGAAACGGCTAGCTGCAGAGTCTCTAGA 60
 DB ||||||||||||||||||
 507 TTGTACCGAAGAGATGAGACCAATCCAGGTGAAAGAAACGGCTAGCTGCAGAGTCTCTAGA 566
 QY 61 TTCCCGAAGACAGTACCCCGAGGAACCTGCTCTCTGACATCGCGCTTCTACTCTCAGAGAAAT 120
 DB ||||||||||||||||||
 567 TTCCCGAAGACAGTACCCCGAGGAACCTGCTCTCTGACATCGCGCTTCTACTCTCAGAGAAAT 626
 QY 121 ACACGGATACAGCTAGTGTGTGACAAATCAGTTTGGATTAGAGGAAGAGAAATATATATC 180
 DB ||||||||||||||||||
 627 ACACGGATACAGCTAGTGTGTGACAAATCAGTTTGGATTAGAGGAAGAGAAATATATATC 686
 QY 181 TGTAGTATGATTTTGTGAAAGTTGAGATATATCCGAAACACAGTACCATTATTATAGAGA 240
 DB ||||||||||||||||||
 687 TGTAGTATGATTTTGTGAAAGTTGAGATATATCCGAAACACAGTACCATTATTATAGAGA 746
 QY 241 CGATGGTGTGGACACAAAGGAAGTTCTCTCAAGGATAAAATCAAGAACGAAACCAATTTAA 300
 DB ||||||||||||||||||
 747 CGATGGTGTGGACACAAAGGAAGTTCTCTCAAGGATAAAATCAAGAACGAAACCAATTTAA 806
 QY 301 ATCATTTCAGTCCGATGACTACTTTGTGCTAAACCTGGATTCAAGATTATTATTTCT 360
 DB ||||||||||||||||||
 807 ATCATTTCAGTCCGATGACTACTTTGTGCTAAACCTGGATTCAAGATTATTATTTCT 866
 QY 361 TTGCTGGAAGATTTCCAAACCGCAGCAGCTTTCAGAGACCAACTGGGAATCTGTCAACAGC 420
 DB ||||||||||||||||||
 867 TTGCTGGAAGATTTCCAAACCGCAGCAGCTTTCAGAGACCAACTGGGAATCTGTCAACAGC 926
 QY 421 TCTATTTCAGGGGTATCCTATAAATCTCTCAATCAGTAAACGGATCCCACTCTGATTGCGGAT 480
 DB ||||||||||||||||||
 927 TCTATTTCAGGGGTATCCTATAAATCTCTCAATCAGTAAACGGATCCCACTCTGATTGCGGAT 986
 QY 481 GCTCTGGACAAAAAATTTGAGAAATTTGATACAGTGGAAAGTCTGCTCAAGTACTTCAAT 540
 DB ||||||||||||||||||
 987 GCTCTGGACAAAAAATTTGAGAAATTTGATACAGTGGAAAGTCTGCTCAAGTACTTCAAT 1046
 QY 541 CCAGAGTCATGGCAAGAAAGATCTTTGAGAAATATGATCTGGACACCCCTCGGTATCGAGGC 600
 DB ||||||||||||||||||
 1047 CCAGAGTCATGGCAAGAAAGATCTTTGAGAAATATGATCTGGACACCCCTCGGTATCGAGGC 1106
 QY 601 AGGTATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
 DB ||||||||||||||||||
 1107 AGGTATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 1166
 QY 661 CGTTTACAGTTGCTACTCCCGAGGAATTTACTCGGTCAATATAAGAGAAAGAGCTGAAGTTGCGC 720
 DB ||||||||||||||||||
 1167 CGTTTACAGTTGCTACTCCCGAGGAATTTACTCGGTCAATATAAGAGAAAGAGCTGAAGTTGCGC 1226
 QY 721 AATGTGCTTCTTTTCCACGTTGCTCTCTGTCAGCGCTGTGGAGGAAATTTGTGGCTGT 780
 DB ||||||||||||||||||
 1227 AATGTGCTTCTTTTCCACGTTGCTCTCTGTCAGCGCTGTGGAGGAAATTTGTGGCTGT 1286
 QY 781 GGAATCTCACTGGAGGCTCTGACATGCAATTCAGGGAACCCGTGAAAGATATCAT 840
 DB ||||||||||||||||||
 1287 GGAATCTCACTGGAGGCTCTGACATGCAATTCAGGGAACCCGTGAAAGATATCAT 1346
 QY 841 GAGGTATTTACAGTTTGGACCTGGCCACATCAAGAGGAGGGGTAGAGTAAAGACCATGGCT 900
 DB ||||||||||||||||||
 1347 GAGGTATTTACAGTTTGGACCTGGCCACATCAAGAGGAGGGGTAGAGTAAAGACCATGGCT 1406
 QY 901 CTAGTTGACATCCAGTTTGGATTCACATGAACGATGATTTCTGACAGTCAAGACCA 960
 DB ||||||||||||||||||
 1407 CTAGTTGACATCCAGTTTGGATTCACATGAACGATGATTTCTGACAGTCAAGACCA 1466
 QY 961 CCTCGATAAGAGATGTCACATCCTTACATTAAAGCTGAAAGAACCTTTAGTTTAAAGGA 1020
 DB ||||||||||||||||||
 1467 CCTCGATAAGAGATGTCACATCCTTACATTAAAGCTGAAAGAACCTTTAGTTTAAAGGA 1526
 QY 1021 GGGTGTAGATAAGAGACCTTTTCTTACCAGAACCAAACTTACTACTAGCTTCAATGCA 1080
 DB ||||||||||||||||||
 1527 GGGTGTAGATAAGAGACCTTTTCTTACCAGAACCAAACTTACTACTAGCTTCAATGCA 1586
 QY 1081 ATGNAACAAGTGGTGTGCTGAGTCTCAGCCTTCTGTTTAAATGCCCATGCCAAGTAGAAA 1140

Query Match 98.9%; Score 1913.6; DB 6; Length 4001; Best Local Similarity 99.4%; Pred. No. 0; Matches 1923; Conservative 7; Mismatches 1; Indels 3; Gaps 1;									
QY	1	TTGTACCGAAGATGAGACCATCCAGGTGAAGGAAACGGCTACGTGAGAGTCTCTAGA	60	Db	1527	GGGTGAGATAAGAGACCCCTTTCTTACCAAGCAACAACTTACTACTAGCCTGCAATGCA	1586		
Db	507	TTGTACCGAAGATGAGACCATCCAGGTGAAGGAAACGGCTACGTGAGAGTCTCTAGA	566	QY	1081	ATGAACACAAGTGGTGTGAGTCTCAGCCTTGTCTTGTATATGCGCATGCGCAAGTAGAAA	1140		
QY	61	TTCCCGAACAGCTACCCAGGAACCTGCTCTCTGACATGCGCGCTTCACTCTCAGGAGAAAT	120	Db	1587	ATGAACACAAGTGGTGTGAGTCTCAGCCTTGTCTTGTATATGCGCATGCGCAAGTAGAAA	1646		
Db	567	TTCCCGAACAGCTACCCAGGAACCTGCTCTCTGACATGCGCGCTTCACTCTCAGGAGAAAT	626	QY	1141	GGTATATCATCAACTCTATACCTAAAGATAATAGGATTCGATTTAAATAATAGTGTTCAG	1200		
QY	121	ACACGGATACAGCTAGTGTGTTGACAAATCAGTTTGGATTAGAGGAAACGAGAAATGATATC	180	Db	1647	GGTATATCATCAACTCTATACCTAAAGATAATAGGATTCGATTTAAATAATAGTGTTCAG	1706		
Db	627	ACACGGATACAGCTAGTGTGTTGACAAATCAGTTTGGATTAGAGGAAACGAGAAATGATATC	686	QY	1201	GTATATATGCAACAAACACACACAGAAATATATTTCATGTCTATGTGTATATAGATCAAAAT	1260		
QY	181	TGTAGGTATGATTTTGTGGAGTTGAAGATATATCCGAACCACTGATTCATTTATAGGAA	240	Db	1707	GTATATATGCAACAAACACACACAGAAATATATTTCATGTCTATGTGTATATAGATCAAAAT	1766		
Db	687	TGTAGGTATGATTTTGTGGAGTTGAAGATATATCCGAACCACTGATTCATTTATAGGAA	746	QY	1261	GTATATATGCAACAAACACACAGGTACACAGAGCTTACATATGTTTGTAGTACACTCT	1320		
QY	241	CGATGTTGGACACAAGGAAGTTCTCTCCAAAGGATAAAATCAAGAACGAAACCAAAATTTAA	300	Db	1767	GTATATATGCAACAAACACACAGGTACACAGAGCTTACATATGTTTGTAGTACACTCT	1826		
Db	747	CGATGTTGGACACAAGGAAGTTCTCTCCAAAGGATAAAATCAAGAACGAAACCAAAATTTAA	806	QY	1321	TAAATCCCTTTGCCAAAATAAGGGATGGTCAAAATATATGAAACATGCTTTTAGAAAAATTT	1380		
QY	301	ATCACATTCAGTCCGATGACTACTTTGTGGCTTAAACCTGGATTTCAAGATTTATTTCT	360	Db	1827	TAAATCCCTTTGCCAAAATAAGGGATGGTCAAAATATATGAAACATGCTTTTAGAAAAATTT	1886		
Db	807	ATCACATTCAGTCCGATGACTACTTTGTGGCTTAAACCTGGATTTCAAGATTTATTTCT	866	QY	1381	AGGAGATAAATTTATTTTAAATTTTGAAACACAAAACAATTTTGAATCTTGTCTCTCTTA	1440		
QY	361	TTGCTGGAAGATTTCCAAACCCGAGCAGCTTCAGAGACCACTGGGAATCTGTCAACAGC	420	Db	1887	AGGAGATAAATTTATTTTAAATTTTGAAACACAAAACAATTTTGAATCTTGTCTCTCTTA	1946		
Db	867	TTGCTGGAAGATTTCCAAACCCGAGCAGCTTCAGAGACCACTGGGAATCTGTCAACAGC	926	QY	1441	AAGAAAGCATCTTGTATATTTAAATCAAAAGATGAGGCTTCTTACATATACATCTTAG	1500		
QY	421	TCTATTTTCAAGGGTATCTTAACTCTCCATCAGTAAACGGATCCCACTCTGATTCGGAT	480	Db	1947	AAGAAAGCATCTTGTATATTTAAATCAAAAGATGAGGCTTCTTACATATACATCTTAG	2006		
Db	927	TCTATTTTCAAGGGTATCTTAACTCTCCATCAGTAAACGGATCCCACTCTGATTCGGAT	986	QY	1501	TTGATTTTAAAAAAGGAAAAA- --GGTTTCCAGAGAAAGGCCAAATACCTTAAGCATTTT	1557		
QY	481	GCTCTGGACAAAAATTCAGAAATTTGATACAGTGGAAAGATCTGCTCAAGTACTTCAAT	540	Db	2007	TTGATTTTAAAAAAGGAAAAAATATGTTTCCAGAGAAAGGCCAAATACCTTAAGCATTTT	2066		
Db	987	GCTCTGGACAAAAATTCAGAAATTTGATACAGTGGAAAGATCTGCTCAAGTACTTCAAT	1046	QY	1558	TTCCATGAGAAGCAGCTGCATACCTTACCTATGTGGAAGCTGTAAATAACCTGTCTCCAAAAACA	1617		
QY	541	CCAGAGTCATGGCAAGAGATCTTGAGATATGTATCTGGACACCCCTCGGTATCGAGGC	600	Db	2067	TTCCATGAGAAGCAGCTGCATACCTTACCTATGTGGAAGCTGTAAATAACCTGTCTCCAAAAACA	2126		
Db	1047	CCAGAGTCATGGCAAGAGATCTTGAGATATGTATCTGGACACCCCTCGGTATCGAGGC	1106	QY	1618	TGCCATATATATATAGTCTTTAGAAATTAATTAATCATTTGTTTATGCAATTTTGGTG	1677		
QY	601	AGGTCAATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG	660	Db	2127	TGCCATATATATATAGTCTTTAGAAATTAATTAATCATTTGTTTATGCAATTTTGGTG	2186		
Db	1107	AGGTCAATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG	1166	QY	1678	AGGCATCTTATTCATTTAAACACCTATCTCAAAACCTTACTTAGAAGGTTTTTTTATTATA	1737		
QY	661	CGTTACAGTTGCACTCCCAAGGAATTAATCGGTCAATATAGAGAGAGCTGAAGTTGGCC	720	Db	2187	AGGCATCTTATTCATTTAAACACCTATCTCAAAACCTTACTTAGAAGGTTTTTTTATTATA	2246		
Db	1167	CGTTACAGTTGCACTCCCAAGGAATTAATCGGTCAATATAGAGAGAGCTGAAGTTGGCC	1226	QY	1738	GTCTCAAAAGACAATGTATAAGCTGTAAACAGAAATTTTGAATTTGTTTCTTTTCCAAAA	1797		
QY	721	AATGTGGTCTTTTCCAGTTGCTCTCTGTCAGCGCTGTGGAGGAAATTTGTGGCTGT	780	Db	2247	GTCTCAAAAGACAATGTATAAGCTGTAAACAGAAATTTTGAATTTGTTTCTTTTCCAAAA	2306		
Db	1227	AATGTGGTCTTTTCCAGTTGCTCTCTGTCAGCGCTGTGGAGGAAATTTGTGGCTGT	1286	QY	1798	CCCTCCCAAAAGCAAATCCCTTCAAGAAATGGCATGGGCATTCGTATGAACCTTTTCCA	1857		
QY	781	GGAACTGTCAACTGGAGTCTGTCACATGCAATTCAGGGAACCGTGAAGAAATGATCAT	840	Db	2307	CCCTCCCAAAAGCAAATCCCTTCAAGAAATGGCATGGGCATTCGTATGAACCTTTTCCA	2366		
Db	1287	GGAACTGTCAACTGGAGTCTGTCACATGCAATTCAGGGAACCGTGAAGAAATGATCAT	1346	QY	1858	GATGGTGTTCAGTGAAGAGTGGGTAGTTCAGAACTTAAAGAGTGAACATTTGAAACATC	1917		
QY	841	GAGGTATTACAGTTTGAGCTGGCCACATCAAGAGAGGGGTAGAGCTAAGACCATGGCT	900	Db	2367	GATGGTGTTCAGTGAAGAGTGGGTAGTTCAGAACTTAAAGAGTGAACATTTGAAACATC	2426		
Db	1347	GAGGTATTACAGTTTGAGCTGGCCACATCAAGAGAGGGGTAGAGCTAAGACCATGGCT	1406	QY	1918	GACGTAACCTGAAA 1931			
QY	901	CTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTTGATCTGCGAGCTCAAGACCA	960	Db	2427	GACGTAACCTGAAA 2440			
Db	1407	CTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTTGATCTGCGAGCTCAAGACCA	1466	RESULT 6					
QY	961	CCTCGATAAGAGAAATGTGCATCTCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAAGGA	1020	ID ADG65192					
Db	1467	CCTCGATAAGAGAAATGTGCATCTCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAAGGA	1526	ADG65192 standard; DNA; 3739 BP.					
QY	1021	GGGTGAGATAAGAGACCCCTTTTCTTACCAGCAACCAAACTTACTACTAGCCTGCAATGCA	1080	XX ADG65192;					
				XX 11-MAR-2004 (first entry)					
				XX Cell proliferation factor Fwa267 encoding sequence.					

XX cell proliferation factor; Fwa267; cardiant; vasotropic;
KW angiocardioopathy; ds.
XX

OS Homo sapiens.

XX WO2000268640-A1.

XX 06-SEP-2002.

XX 28-FEB-2002; 2002WO-CN000126.

XX 28-FEB-2001; 2001CN-00109260.

XX (FUWA-) FU WAI HOSPITAL CHINESE ACAD MEDICAL SCI.

XX Hui R, Chen J, Liu B, Liu Y;

XX WPI; 2003-058305/05.

DR P-PSDB; ADG65193.

XX Human-originated cell proliferation factor Fwa267 polypeptide, and the
PT polypeptide encoding it, applicable in diagnosis and treatment of
PT angiocardioopathy.

XX Claim 5; SEQ ID NO 1; 46pp; Chinese.

XX The present invention relates to an isolated cell proliferation factor
CC Fwa267 polynucleotide which is cardiant and vasotropic in its action. The
CC polypeptide and its encoded polynucleotide are applicable in the
CC diagnosis and treatment of angiocardioopathy. The polypeptide is useful
CC for producing drug compositions for treating angiocardioopathy. The
CC present sequence represents the human cell proliferation factor Fwa267
CC encoding sequence.

XX Sequence 3739 BP; 1175 A; 732 C; 713 G; 1119 T; 0 U; 0 Other;

XX Query Match 98.9%; Score 1913.2; DB 10; Length 3739;

XX Best Local Similarity 99.7%; Pred. No. 0;

XX Matches 1928; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

QY 1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAGAAACGGCTAGCTCAGAGTCTTAGA 60

DB 251 TTGTACCGAAGAGATGAGACCATCCAGGTGAAGAAACGGCTAGCTCAGAGTCTTAGA 310

QY 61 TTCCCGAAGACGCTACCCAGGAACTGCTCCTGACATGGCGCTTCACTCTCAGGAGAT 120

DB 311 TTCCCGAAGACGCTACCCAGGAACTGCTCCTGACATGGCGCTTCACTCTCAGGAGAT 370

QY 121 ACACGGATACAGTGTGTTGACCAATCAGTTTGGATTAGAGGAAGCAAAATGATATC 180

DB 371 ACACGGATACAGTGTGTTGACCAATCAGTTTGGATTAGAGGAAGCAAAATGATATC 430

QY 181 TGTAGGTATGATTTGTGGAAGTTGAAGATATATCCGAAACCCAGTACCAATTATAGAGA 240

DB 431 TGTAGGTATGATTTGTGGAAGTTGAAGATATATCCGAAACCCAGTACCAATTATAGAGA 490

QY 241 CGATGGTGGACACAAGGAGTTCCTCCAGGATAAATCAAGAACCAACCAAAATTA 300

DB 491 CGATGGTGGACACAAGGAGTTCCTCCAGGATAAATCAAGAACCAACCAAAATTA 550

QY 301 ATCACAATTCAGTCCGATGACTTCTTGGCTAAACCTGGATTCAAGATTTATTATTCT 360

DB 551 ATCACAATTCAGTCCGATGACTTCTTGGCTAAACCTGGATTCAAGATTTATTATTCT 610

QY 361 TTGCTGGAAGATTTCCAAACCCAGCAGCTTCAGAGACCAATCGGAATCTGTCAAGC 420

DB 611 TTGCTGGAAGATTTCCAAACCCAGCAGCTTCAGAGACCAATCGGAATCTGTCAAGC 670

QY 421 TCTATTTTCAAGGGTATCCTTAACCTCCATCAGTAAACGGATCCCACTCTGATTCGGAT 480

DB 671 TCTATTTTCAAGGGTATCCTTAACCTCCATCAGTAAACGGATCCCACTCTGATTCGGAT 730

QY 481 GCTCTGGACAAAAAATTGACAGAAATTGATACAGTGAAGATCTGCTCAAGTACTTCAAT 540

DB 731 GCTCTGGACAAAAAATTGACAGAAATTGATACAGTGAAGATCTGCTCAAGTACTTCAAT 790

QY 541 CCAGAGTCATGGCAAGAAAGATCTTGAGAAATATGATCTGGACACCCCTCGGTATCGAGGC 600

DB 791 CCAGAGTCATGGCAAGAAAGATCTTGAGAAATATGATCTGGACACCCCTCGGTATCGAGGC 850

QY 601 AGGTCATACCATGACCCGAAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660

DB 851 AGGTCATACCATGACCCGAAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 910

QY 661 CGTTACAGTTGCACTCCACAGGAATTACTCGGTCAATATAAGAGAGAGCTGAAGTTGSCC 720

DB 911 CGTTACAGTTGCACTCCACAGGAATTACTCGGTCAATATAAGAGAGAGCTGAAGTTGSCC 970

QY 721 AATGTGCTCTTCTTTCCACGTTGCTCTGCTGAGCGCTGTGAGGAAATTTGTGGCTGT 780

DB 971 AATGTGCTCTTCTTTCCACGTTGCTCTGCTGAGCGCTGTGAGGAAATTTGTGGCTGT 1030

QY 781 GGAACTGTCAACTGGAGGCTCTGCACATGCAATTCAGGGAACCCGTGAAAAAGTATCAT 840

DB 1031 GGAACTGTCAACTGGAGGCTCTGCACATGCAATTCAGGGAACCCGTGAAAAAGTATCAT 1090

QY 841 GAGGTATTACAGTTTGGACCTGGCCACATCAAGAGAGGGGTAGAGCTTAAGACCATGCT 900

DB 1091 GAGGTATTACAGTTTGGACCTGGCCACATCAAGAGAGGGGTAGAGCTTAAGACCATGCT 1150

QY 901 CTAGTTCACATCCAGTTGGATTCACATGAACGATGCGATTTGATCTGCGCTCAAGACCA 960

DB 1151 CTAGTTCACATCCAGTTGGATTCACATGAACGATGCGATTTGATCTGCGCTCAAGACCA 1210

QY 961 CCTCGATAAGAGAAATGTGCACATCCTTTACATTAAGCCTGAAAGAACCTTTAGTTAAGGA 1020

DB 1211 CCTCGATAAGAGAAATGTGCACATCCTTTACATTAAGCCTGAAAGAACCTTTAGTTAAGGA 1270

QY 1021 GGGTGAGATAAGAGACCTTTTCTACCGCAACCAAACTTACTACTAGCTGCAATGCA 1080

DB 1271 GGGTGAGATAAGAGACCTTTTCTACCGCAACCAAACTTACTACTAGCTGCAATGCA 1330

QY 1081 ATGAACAACAGTGTGCTGAGTCTCAGCCTTGTGTTGTAATGCGCAATGCAAGTAGAAA 1140

DB 1331 ATGAACAACAGTGTGCTGAGTCTCAGCCTTGTGTTGTAATGCGCAATGCAAGTAGAAA 1390

QY 1141 GGTATATCATCAACTTCTATACCTAAGAATATAGGATGCAATTAATAATAGTTGTTGAG 1200

DB 1391 GGTATATCATCAACTTCTATACCTAAGAATATAGGATGCAATTAATAATAGTTGTTGAG 1450

QY 1201 GTTATATGACAAAACACACACAGAAATATATTCAATGCTATGTGTATATAGATCAAT 1260

DB 1451 GTTATATGACAAAACACACACAGAAATATATTCAATGCTATGTGTATATAGATCAAT 1510

QY 1261 GTTTTTTTTGGTATATATAACAGGTACACAGAGCTTACATATGTTTGGTTAGTTAGACTCT 1320

DB 1511 GTTTTTTTTGGTATATATAACAGGTACACAGAGCTTACATATGTTTGGTTAGTTAGACTCT 1570

QY 1321 TAAATTCCTTTTGGCAAAATAGGGATGGTCAAAATATATGAACACATGCTTTTAGAAAAATTT 1380

DB 1571 TAAATTCCTTTTGGCAAAATAGGGATGGTCAAAATATATGAACACATGCTTTTAGAAAAATTT 1630

QY 1381 AGGAGATAAATTTATTTTAAATTTTGAACAACAAAATTTTGAATCTTGCTCTCTTA 1440

DB 1631 AGGAGATAAATTTATTTTAAATTTTGAACAACAAAATTTTGAATCTTGCTCTCTTA 1690

QY 1441 AAGAAAGCATCTGTATATTAATAAATCAAAAGATGAGCTTTCTTACATATACATCTTAG 1500

DB 1691 AAGAAAGCATCTGTATATTAATAAATCAAAAGATGAGCTTTCTTACATATACATCTTAG 1750

QY 1501 TTGATTTTAAAAAAGGAAAAA---GGTTTCCAGAGAAAAAGGCCAATACCTAAGCATTTT 1557

DB 1751 TTGATTTTAAAAAAGGAAAAAATATGGTTTCCAGAGAAAAAGGCCAATACCTAAGCATTTT 1810

QY 1558 TTCCATGAGAGACATGCAATCTTACTTATGTGAGCTGTAATAACCTGCTCTCCAAAACCA 1617

Db 1811 TTCCATGAGAAGCAGTGCATACCTTACCTATGTGGACTATAATAACCTGTCTCCAAAACCA 1870
Qy 1618 TGCATAATAATATAGTGGCTTTAGAAAATTAATCATCTGTTTATGCAATTTTGCTG 1677
Db 1871 TGCATAATAATATAGTGGCTTTAGAAAATTAATCATCTGTTTATGCAATTTTGCTG 1930
Qy 1678 AGGCATCTTATTTCAATTAACACCTATCTCAAAAACCTTACTTGAAGGTTTTTATATA 1737
Db 1931 AGGCATCTTATTTCAATTAACACCTATCTCAAAAACCTTACTTGAAGGTTTTTATATA 1990
Qy 1738 GTCTTCAAAAAGACAAATGATAGCTGTAAACAGAAATTTGAATGTTTCTTTTGCAAA 1797
Db 1991 GTCTTCAAAAAGACAAATGATAGCTGTAAACAGAAATTTGAATGTTTCTTTTGCAAA 2050
Qy 1798 CCCTCCCAAAAGCAAAATCCCTTCAAGAAATGGCATGGCATCTGTATGAACCTTCCA 1857
Db 2051 CCCTCCCAAAAGCAAAATCCCTTCAAGAAATGGCATGGCATCTGTATGAACCTTCCA 2110
Qy 1858 GATGGTGTTCAGTGAAGATGTGGGTAGTTGAGAACTTAAAAAGTCAACATTTGAACATC 1917
Db 2111 GATGGTGTTCAGTGAAGATGTGGGTAGTTGAGAACTTAAAAAGTCAACATTTGAACATC 2170
Qy 1918 GACGTAACCTGGAAA 1931
Db 2171 GACGTAACCTGGAAA 2184

RESULT 7
AD020112
ID ADO20112 standard; cDNA; 3808 BP.
XX
AC ADO20112;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human PRO polynucleotide #511.
XX
KW Human; PRO; gene; ss; immune related disorder;
KW systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis;
KW juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome;
KW vasculitis; sarcoidosis; autoimmune haemolytic anaemia;
KW autoimmune thrombocytopenia; thyroiditis; diabetes mellitus;
KW renal disease; demyelinating disease; central nervous system;
KW peripheral nervous system; demyelinating polyneuropathy;
KW Guillain-Barre syndrome;
KW chronic inflammatory demyelinating polyneuropathy.
XX
OS Homo sapiens.
XX
PN WO2004043361-A2.
XX
PD 27-MAY-2004.
XX
PF 06-NOV-2003; 2003WO-US035268.
XX
PR 08-NOV-2002; 2002US-0425235P.
XX
PA (GETH) GENENTECH INC.
XX
PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PW;
PI Wood WI, Wu TD;
XX
DR WPI; 2004-420067/39.
XX
P-PSDB; ADO20113.
XX
PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
PT treating an immune related disorder such as systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
PT spondyloarthritis.
XX
PS Claim 1; SEQ ID NO 1076; 1731pp; English.

CC The invention relates to human PRO polypeptides and the polynucleotides
CC encoding them. The polypeptides and polynucleotides are useful for
CC treating and diagnosing immune related disorders in mammals. The immune
CC related disorders include systemic lupus erythematosus, rheumatoid
CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
CC mellitus, immune-mediated renal disease, demyelinating diseases of the
CC central or peripheral nervous system, demyelinating polyneuropathy,
CC Guillain-Barre syndrome and chronic inflammatory demyelinating
CC polyneuropathy. This sequence represents a human PRO polynucleotide of
XX the invention.
Qy Sequence 3808 BP; 1191 A; 750 C; 738 G; 1129 T; 0 U; 0 Other;
Query Match 98.9%; Score 1913.2; DB 12; Length 3808;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1928; Conservative 0; Mismatches 3; Indels 3; Gaps 1;
Qy 1 TTGTACCCGAAGAGATGAGACCATCCAGGTGAAAGAAACGGCTACGTGCAGAGTCTTAGA 60
Db 320 TTGTACCCGAAGAGATGAGACCATCCAGGTGAAAGAAACGGCTACGTGCAGAGTCTTAGA 379
Qy 61 TTCCCGAAACAGTACCCCGAGAACTCTCTCTGACATGGCGGCTTCACTCTCAGAGAAT 120
Db 380 TTCCCGAAACAGTACCCCGAGAACTCTCTCTGACATGGCGGCTTCACTCTCAGAGAAT 439
Qy 121 ACAGGATACAGTAGTGTGTTGACAATCAGTTTGGATTAGAGGAGCAAGAAATCATATC 180
Db 440 ACAGGATACAGTAGTGTGTTGACAATCAGTTTGGATTAGAGGAGCAAGAAATCATATC 499
Qy 181 TGTAGGTATGATTTTGTGGAAGTTGAAAGATATATCCGAAACAGTACCATTTATAGAGGA 240
Db 500 TGTAGGTATGATTTTGTGGAAGTTGAAAGATATATCCGAAACAGTACCATTTATAGAGGA 559
Qy 241 CGATGGTGTGACACAAAGAAAGTTCTCCAAAGGATAAAATCAAGAACGAAACCAATTTAA 300
Db 560 CGATGGTGTGACACAAAGAAAGTTCTCCAAAGGATAAAATCAAGAACGAAACCAATTTAA 619
Qy 301 ATCATTTCAGTCCGATGACTTCTTGTGGCTAAACCTGGATTCAAGATTATTTATCT 360
Db 620 ATCATTTCAGTCCGATGACTTCTTGTGGCTAAACCTGGATTCAAGATTATTTATCT 679
Qy 361 TTGCTGGAAGATTTCCAAACCGCAGCAGCTTTCAGAGACCAACTGGGAATCTGTCAACAGC 420
Db 680 TTGCTGGAAGATTTCCAAACCGCAGCAGCTTTCAGAGACCAACTGGGAATCTGTCAACAGC 739
Qy 421 TCTATTTTCAGGGGTATCTTATACTCTCCATCAGTAACGGATCCCACTCTGATTGCGGAT 480
Db 740 TCTATTTTCAGGGGTATCTTATACTCTCCATCAGTAACGGATCCCACTCTGATTGCGGAT 799
Qy 481 GCTCTGGACAAAATAATTCAGAAATTTGATACAGTGGGAAGATCTGCTCAAGTACTTCAAT 540
Db 800 GCTCTGGACAAAATAATTCAGAAATTTGATACAGTGGGAAGATCTGCTCAAGTACTTCAAT 859
Qy 541 CCAGAGTCATGGCAAGAAAGATCTTTGAGAATATGTATCTGGACACCCCTCGGTATCGAGGC 600
Db 860 CCAGAGTCATGGCAAGAAAGATCTTTGAGAATATGTATCTGGACACCCCTCGGTATCGAGGC 919
Qy 601 AGGTATACATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
Db 920 AGGTATACATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 979
Qy 661 GGTTCAGAGTTGCTCTCCAGGAATTTACTCGGTCAATATAGAGAAAGAGCTCAAGTTGGCC 720
Db 980 GGTTCAGAGTTGCTCTCCAGGAATTTACTCGGTCAATATAGAGAAAGAGCTCAAGTTGGCC 1039
Qy 721 AATGTGTTCTTTTCCACGTTGCTCTCTCGTGCAGCGCTGTGGAGAAATTTGGTGTGT 780
Db 1040 AATGTGTTCTTTTCCACGTTGCTCTCTCGTGCAGCGCTGTGGAGAAATTTGGTGTGT 1099
Qy 781 GGAATCTCACTGGAGGTCTCTGCACATCAATTTTCAGGAAACCGTGAAGAAATTCAT 840

Db 1100 GGAACGTCTCACTGGAGGCTCTGCACATGCAATTCAGGGAAAACCGTGAAAAAGTATCAT 1159

Qy 841 GAGGTATTTACAGTTTGGAGCTGGCCACATCAAGAGGGGGTAGAGCTAAGACCATGGCT 900

Db 1160 GAGGTATTTACAGTTTGGAGCTGGCCACATCAAGAGGGGGTAGAGCTAAGACCATGGCT 1219

Qy 901 CTAGTTGACATCCAGTTGGATCAGCATGAAGCATGCGATTGTATCTGAGCTCAAGACCA 960

Db 1220 CTAGTTGACATCCAGTTGGATCAGCATGAAGCATGCGATTGTATCTGAGCTCAAGACCA 1279

Qy 961 CCTCGATAAGAGATGTGCACATCCTTACATTAAGCCCTGGAAGAACCTTTAGTTTAAAGGA 1020

Db 1280 CCTCGATAAGAGATGTGCACATCCTTACATTAAGCCCTGGAAGAACCTTTAGTTTAAAGGA 1339

Qy 1021 GGGTGAGATAAGAGACCCCTTTCTTACCAGCAACCAAACTTACTACTAGCCCTGCAATGCA 1080

Db 1340 GGGTGAGATAAGAGACCCCTTTCTTACCAGCAACCAAACTTACTACTAGCCCTGCAATGCA 1399

Qy 1081 ATGAACACAAGTGTGCTGAGTCTCAGCCCTGCTTGTGTTAATGCCATGGCAAGTAGAAAA 1140

Db 1400 ATGAACACAAGTGTGCTGAGTCTCAGCCCTGCTTGTGTTAATGCCATGGCAAGTAGAAAA 1459

Qy 1141 GGTATATCATCAACTCTTATACCTTAAGATATAGGATTTGCATTTAATAATAGTCTTTGAG 1200

Db 1460 GGTATATCATCAACTCTTATACCTTAAGATATAGGATTTGCATTTAATAATAGTCTTTGAG 1519

Qy 1201 GTTATATATGCACAAACACACACAGAAATATATTCATGCTCTATGTGTATATAGATCAAAAT 1260

Db 1520 GTTATATATGCACAAACACACACAGAAATATATTCATGCTCTATGTGTATATAGATCAAAAT 1579

Qy 1261 GTTTTTTTTGGTATATATAACACAGGTACACAGAGCTTACATATGTTTGGTTAGTTAGACTCT 1320

Db 1580 GTTTTTTTTGGTATATATAACACAGGTACACAGAGCTTACATATGTTTGGTTAGTTAGACTCT 1639

Qy 1321 TAAATCTTTTCCAAATAGGATGCTCAATATATAGAAATGCAATGCTTTTAGAAAAATTT 1380

Db 1640 TAAATCTTTTCCAAATAGGATGCTCAATATATAGAAATGCAATGCTTTTAGAAAAATTT 1699

Qy 1381 AGGAGATAAAATTTTAAATTTTGAACACAAAAAAATTTTGAATCTTGTCTCTCTTA 1440

Db 1700 AGGAGATAAAATTTTAAATTTTGAACACAAAAAAATTTTGAATCTTGTCTCTCTTA 1759

Qy 1441 AAGAAAGCATCTGTATATTAATAATCAAAAGATGAGGCTTCTTACATATACATCTTTAG 1500

Db 1760 AAGAAAGCATCTGTATATTAATAATCAAAAGATGAGGCTTCTTACATATACATCTTTAG 1819

Qy 1501 TTGATTATTAATAAGGAABAAA---GGTTTCCAGAGAAAGGCCAAATACCTAAGCATTTT 1557

Db 1820 TTGATTATTAATAAGGAABAAAATATGGTTTCCAGAGAAAGGCCAAATACCTAAGCATTTT 1879

Qy 1558 TTCCATGAGAGCACTGCATATCTTACCTATGTGGACTGTATAACCTGCTCTCCAAAACCA 1617

Db 1880 TTCCATGAGAGCACTGCATATCTTACCTATGTGGACTGTATAACCTGCTCTCCAAAACCA 1939

Qy 1618 TGCCATAATAATAAGTGTCTTTAGAAATTAATCAATTTGTTTGTATGCAATTTTGGCTG 1677

Db 1940 TGCCATAATAATAAGTGTCTTTAGAAATTAATCAATTTGTTTGTATGCAATTTTGGCTG 1999

Qy 1678 AGGCATCTTTATTCATTTAAACCTATCTCAAAACCTTACTTAGAAGCTTTTATTTATA 1737

Db 2000 AGGCATCTTTATTCATTTAAACCTATCTCAAAACCTTACTTAGAAGCTTTTATTTATA 2059

Qy 1738 GTCCTACAAAAGACAACTGTATAAGCTGTAAACAGAAATTTTGAATTTTCTTTCTTGCAAAA 1797

Db 2060 GTCCTACAAAAGACAACTGTATAAGCTGTAAACAGAAATTTTGAATTTTCTTTCTTGCAAAA 2119

Qy 1798 CCCCTCCAAAAGCAAAATCCCTTCAAGAAATGGCATGGCAATCTGTATGAACCTTTTCCA 1857

Db 2120 CCCCTCCAAAAGCAAAATCCCTTCAAGAAATGGCATGGCAATCTGTATGAACCTTTTCCA 2179

Qy 1858 GATGTGTTTCAGTGAAGATGTGGTAGTTGAGAACTTTAAAAAGTGAACATTTGAACATC 1917

Db 2180 GATGTGTTTCAGTGAAGATGTGGTAGTTGAGAACTTTAAAAAGTGAACATTTGAACATC 2239

Qy 1918 GACGTAACCTGAAAA 1931

Db 2240 GACGTAACCTGAAAA 2253

RESULT 8

AAH46939

ID AAH46939 standard; cDNA; 3798 BP.

XX

AC AAH46939;

XX

DT 25-SEP-2001 (first entry)

XX

Human secreted protein encoding cDNA (clone Id HGCNC48).

DE

XX

Secreted protein; immunosuppressive; antiarthritic; antirheumatic;

XX

antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;

XX

neotropic; neuroprotective; antibacterial; virucide; fungicide; human;

XX

opthalmological; gene therapy; ss.

OS Homo sapiens.

XX

W0200155430-A1.

PN

XX

02-AUG-2001.

PD

XX

17-JAN-2001; 2001WO-US001431.

XX

31-JAN-2000; 2000US-0179065P.

PR

XX

04-FEB-2000; 2000US-0180628P.

PR

XX

12-SEP-2000; 2000US-0231968P.

PR

XX

(HUMA-) HUMAN GENOME.SCI INC.

PA

XX

Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR;

PI

XX

Olsen HS, Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH;

PI

XX

Fiscella M, Ni J, Ruben SM, Barash SC;

DR

XX

WPI; 2001-476220/51.

DR

XX

P-PSDB; AAB85529.

PS

XX

17 isolated nucleic acid molecules encoding human secreted proteins, used

PT

XX

to preventing, treating or ameliorating a medical condition.

PT

XX

Claim 1; Page 417-418; 482pp; English.

PS

XX

The invention provides novel human secreted proteins and polynucleotides

CC

XX

encoding them. The secreted proteins can be expressed by standard

CC

XX

recombinant methodology. The secreted proteins and polynucleotides are

CC

XX

used to prevent, treat or ameliorate a medical condition in e.g. humans,

CC

XX

mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They can

CC

XX

also be used in diagnosing a pathological condition. The antibodies to

CC

XX

the proteins can also be used in alleviating symptoms associated with the

CC

XX

disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme

CC

XX

linked immunoassort assays (ELISA). Disorders which are diagnosed or

CC

XX

treated include autoimmune diseases e.g. rheumatoid arthritis,

CC

XX

hyperproliferative disorders e.g. neoplasms of the breast or liver,

CC

XX

cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders

CC

XX

e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g.

CC

XX

Alzheimer's disease, infections caused by bacteria, viruses and fungi and

CC

XX

ocular disorders e.g. corneal infection. The polypeptides can also be

CC

XX

used to aid wound healing and epithelial cell proliferation, to prevent

CC

XX

skin aging due to sunburn, to maintain organs before transplantation, for

CC

XX

supporting cell culture of primary tissues, to regenerate tissues and in

CC

XX

chemotaxis. The polypeptides can also be used as a food additive or

CC

XX

preservative to increase or decrease storage capabilities. The present

CC

XX

sequence represents a human secreted protein encoding cDNA

XX

Sequence 3798 BP; 1189 A; 749 C; 737 G; 1123 T; 0 U; 0 Other;

SQ

Query Match 98.8%; Score 1911.6; DB 5; Length 3798;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 1927; Conservative 0; Mismatches 4; Indels 3; Gaps 1;			
QY	1	TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGACAGTCTCTAGA	60
Db	310	TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGACAGTCTCTAGA	369
QY	61	TTCCCGAAGCTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAAT	120
Db	370	TTCCCGAAGCTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAAT	429
QY	121	ACACGGATACAGCTAGTGTGTCACATCAGTTGGATTAGAGAAACGAGAAATGATATC	180
Db	430	ACACGGATACAGCTAGTGTGTCACATCAGTTGGATTAGAGAAACGAGAAATGATATC	489
QY	181	TGTAGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCAAGTACCAATATTAGAGGA	240
Db	490	TGTAGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCAAGTACCAATATTAGAGGA	549
QY	241	CGATGTTGTGGAACAAGGAAGTTCTCCAAAGGATAAATCAAGAACGAAACCAATTTAA	300
Db	550	CGATGTTGTGGAACAAGGAAGTTCTCCAAAGGATAAATCAAGAACGAAACCAATTTAA	609
QY	301	ATCACATTCAGTCCGATGACTACTTTGTGGCTTAAACCTGGATTCAAGATTATTATCT	360
Db	610	ATCACATTCAGTCCGATGACTACTTTGTGGCTTAAACCTGGATTCAAGATTATTATCT	669
QY	361	TTGCTGGAAGATTTCCAACCCGAGCAGCTTCAGAGACCAACTGGGAATCTGTCAACAGC	420
Db	670	TTGCTGGAAGATTTCCAACCCGAGCAGCTTCAGAGACCAACTGGGAATCTGTCAACAGC	729
QY	421	TCATTTTCAGGGTATCCTATAACTCTCCATCAGTAACCGATCCCACTCTGATTCGGAT	480
Db	730	TCATTTTCAGGGTATCCTATAACTCTCCATCAGTAACCGATCCCACTCTGATTCGGAT	789
QY	481	GCTCTGGAACAAAAATTCAGAAATTTGATACAGTGGAGATCTGCTCAAGTACTTCAAT	540
Db	790	GCTCTGGAACAAAAATTCAGAAATTTGATACAGTGGAGATCTGCTCAAGTACTTCAAT	849
QY	541	CCAGAGTCATGCGAAGAATCTTGAGAATATGTATCTGGACACCCCTCGGTATCGAGGC	600
Db	850	CCAGAGTCATGCGAAGAATCTTGAGAATATGTATCTGGACACCCCTCGGTATCGAGGC	909
QY	601	AGGTATACATGACCGGAGTCAAAAGTTGACCTGGATAGGCTCATGATGATGCCAAG	660
Db	910	AGGTATACATGACCGGAGTCAAAAGTTGACCTGGATAGGCTCATGATGATGCCAAG	969
QY	661	CGTTACAGTTGCACTCCAGGAATTAACCTCGTCAATATAAGAGAAGAGCTGAAGTTGGCC	720
Db	970	CGTTACAGTTGCACTCCAGGAATTAACCTCGTCAATATAAGAGAAGAGCTGAAGTTGGCC	1029
QY	721	AATGTGGTCTTCTTCCAGTTCCTCTCGTGCAGCGCTGTGGAGAAATTTGGCTGT	780
Db	1030	AATGTGGTCTTCTTCCAGTTCCTCTCGTGCAGCGCTGTGGAGAAATTTGGCTGT	1089
QY	781	GGAACTGTCAACTGGAGTCTGACATGCAATTCAGGAAACCGTGAAGATATCAT	840
Db	1090	GGAACTGTCAACTGGAGTCTGACATGCAATTCAGGAAACCGTGAAGATATCAT	1149
QY	841	GAGGTATTACAGTTTGAGCTGCGCAATCAAGAGAGGGGTAGAGCTAAGACCATGGCT	900
Db	1150	GAGGTATTACAGTTTGAGCTGCGCAATCAAGAGAGGGGTAGAGCTAAGACCATGGCT	1209
QY	901	CTAGTTGACATCCAGTTGGATCACCATGAACGATGCTGTCGAGGAAATTTGGCTGT	960
Db	1210	CTAGTTGACATCCAGTTGGATCACCATGAACGATGCTGTCGAGGAAATTTGGCTGT	1269
QY	961	CCTCGATAGAGATGTGCACATCCTTACATTAAGCTGAAGAACCTTTAGTTTAAAGA	1020
Db	1270	CCTCGATAGAGATGTGCACATCCTTACATTAAGCTGAAGAACCTTTAGTTTAAAGA	1329
QY	1021	GGGTGAGATAAGAGACCTTTTCTACCAAGCAACCAACTTACTACTAGCCTGCAATGCA	1080
Db	1330	GGGTGAGATAAGAGACCTTTTCTACCAAGCAACCAACTTACTACTAGCCTGCAATGCA	1389

QY	1081	ATGAACACAAAGTGGTTGCTGAGTCTCAGCCTTGTCTTCTTAATGCGCATGCGAAGTAGAAA	1140
Db	1390	ATGAACACAAAGTGGTTGCTGAGTCTCAGCCTTGTCTTCTTAATGCGCATGCGAAGTAGAAA	1449
QY	1141	GGTATATCATCAACTTCTATACCTAAAGAAATAGGATTGCAATTTAATAATAGTGTTCGAG	1200
Db	1450	GGTATATCATCAACTTCTATACCTAAAGAAATAGGATTGCAATTTAATAATAGTGTTCGAG	1509
QY	1201	GTTATATATGACAAACACACACAGAAATATATTATGCTCTATGTTGTTATATAGATCAAA	1260
Db	1510	GTTATATATGACAAACACACAGAAATATATTATGCTCTATGTTGTTATATAGATCAAA	1569
QY	1261	GTTTTTTTTTGGTATATATAACAGGTACACAGAGCTTACATATGTTTGGTGTAGTACTCT	1320
Db	1570	GTTTTTTTTTGGTATATATAACAGGTACACAGAGCTTACATATGTTTGGTGTAGTACTCT	1629
QY	1321	TAAATCCTTTGCCAAAATAAGGGATGGTCAAAATATATGAACACATGCTTTTAGAAAATTT	1380
Db	1630	TAAATCCTTTGCCAAAATAAGGGATGGTCAAAATATATGAACACATGCTTTTAGAAAATTT	1689
QY	1381	AGGATATAAATTTATTTTAAATTTTGAACACAAACAAATTTTGAATCTTGCTCTCTTA	1440
Db	1690	AGGATATAAATTTATTTTAAATTTTGAACACAAACAAATTTTGAATCTTGCTCTCTTA	1749
QY	1441	AAGAAAGCATCTTGATATATAAATCAAAAGATGAGGCTTTCTTACATATACATCTTTAG	1500
Db	1750	AAGAAAGCATCTTGATATATAAATCAAAAGATGAGGCTTTCTTACATATACATCTTTAG	1809
QY	1501	TTGATTTATAAAAAAGGAAAAA---GGTTTCCAGAGAAAAGGCCAAATACCTTAAGCATTTT	1557
Db	1810	TTGATTTATAAAAAAGGAAAAAATATGGTTTCCAGAGAAAAGGCCAAATACCTTAAGCATTTT	1869
QY	1558	TTCCATGAGAGAGCACTGCATCTTACCTATGTGAGCTGTAAATACCTGTCTCCAAAACCA	1617
Db	1870	TTCCATGAGAGAGCACTGCATCTTACCTATGTGAGCTGTAAATACCTGTCTCCAAAACCA	1929
QY	1618	TGCCATAATATAAAGTGGCTTTAGAAAATTAATCATTTGTTTATGCAATTTTGGCTG	1677
Db	1930	TGCCATAATATAAAGTGGCTTTAGAAAATTAATCATTTGTTTATGCAATTTTGGCTG	1989
QY	1678	AGGCATCTTTATTCATTTAACCTTCTCMAAACTTACTTAGAAGGTTTTTTTATTATA	1737
Db	1990	AGGCATCTTTATTCATTTAACCTTCTCMAAACTTACTTAGAAGGTTTTTTTATTATA	2049
QY	1738	GTCCTACAAAAGACAAATGTATAAGCTGTAAACAGAAATTTTGAATTTGTTTCTTTGCAAAA	1797
Db	2050	GTCCTACAAAAGACAAATGTATAAGCTGTAAACAGAAATTTTGAATTTGTTTCTTTGCAAAA	2109
QY	1798	CCCCCTCCACAAAAGCAAAATCCTTTCAAGAAATGGCATGGCAATCTGTATGAACCTTTCCA	1857
Db	2110	CCCCCTCCACAAAAGCAAAATCCTTTCAAGAAATGGCATGGCAATCTGTATGAACCTTTCCA	2169
QY	1858	GATGGTGTTCAGTGAAGAGATGGGTAGTTGAGAACTTAAAGAGTGAACATTGAAACATC	1917
Db	2170	GATGGTGTTCAGTGAAGAGATGGGTAGTTGAGAACTTAAAGAGTGAACATTGAAACATC	2229
QY	1918	GACCTAACTGGAAA 1931	
Db	2230	GACCTAACTGGAAA 2243	

RESULT 9

ABS58475

ID ABS58475 standard; cDNA; 3798 BP.

XX ABS58475;

AC ABS58475;

XX 05-NOV-2002 (first entry)

XX Human secreted protein encoding cDNA #7.

XX Human; secreted protein; autoimmune disease; blood coagulation disorder;

KW

blood platelet disorder; hyperproliferative disorder; renal disorder; ss;
neurodegenerative disorder; cardiovascular disorder; vascular disorder;
respiratory disorder; endocrine disorder; reproductive disorder; gene;
gastrointestinal disorder; infectious disease; antianaemic; cytosstatic;
antiarrhythmic; immunosuppressive; antiasthmatic; antidiabetic;
antiinflammatory; antipsoriatic; antiparkinsonian; neuroprotective.

XX Homo sapiens.

OS US2002120103-A1.

XX 29-AUG-2002.

XX 27-JUL-2001; 2001US-00915582.

XX 31-JAN-2000; 2000US-0179065P.

XX 04-FEB-2000; 2000US-0180628P.

XX 12-SEP-2000; 2000US-0231968P.

XX 17-JAN-2001; 2001WO-US0001431.

XX (ROSE/) ROSEN C A.

XX (KOMA/) KOMATSUOULIS G A.

XX (BAKE/) BAKER K P.

XX (BIRSE/) BIRSE C E.

XX (SOPP/) SOPPET D R.

XX (OLSEN/) OLSEN H S.

XX (MOOR/) MOORE P A.

XX (WEIP/) WEI P.

XX (EBNE/) EBNER R.

XX (DUAN/) DUAN D R.

XX (SHIY/) SHI Y.

XX (CHOI/) CHOI G H.

XX (FISC/) FISCCELLA M.

XX (NIJ/) NI J.

XX (RUBE/) RUBEN S M.

XX (BARA/) BARASH S C.

XX

PI Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR;

PI Olsen HS, Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH;

PI Fiscella M, Ni J, Ruben SM, Barash SC;

XX WPI; 2002-608160/65.

XX P-PSDB; ABG76575.

XX

PT New secreted polypeptides and encoding polynucleotides, useful for

PT preventing, treating and diagnosing diseases e.g. anemia, cancer,

PT diabetes, asthma, psoriasis, Parkinson's and Alzheimer's.

XX

PS Claim 1; Page 357-359; 238pp; English.

XX

CC The invention relates to an isolated nucleic acid molecule which encodes

CC a human secreted protein. The sequences are useful for diagnosing or

CC diagnosing a susceptibility to a pathological condition in a subject

CC comprising determining the presence or absence of a mutation in the DNA

CC or expression of the protein. The sequences are useful for identifying a

CC binding partner to the protein comprising contacting the protein with a

CC binding partner and determining whether the binding partner effects an

CC activity. The DNA and protein sequences are used for preventing, treating

CC or ameliorating a medical condition such as an autoimmune disease (e.g.

CC multiple sclerosis, myasthenia gravis), blood coagulation disorders (e.g.

CC afibrinogenemia, haemophilia), blood platelet disorders (e.g.

CC thrombocytopenia), hyperproliferative disorders (e.g. sarcoidosis, Sezary

CC syndrome), neurodegenerative disorders (e.g. Alzheimer's disease,

CC Parkinson's disease), renal disorders (e.g. renal vein thrombosis, kidney

CC infarction), cardiovascular disorders (e.g. cardiac arrest,

CC pericarditis), vascular disorders (e.g. aneurysm, ischaemia), respiratory

CC disorders (e.g. tonsillitis, laryngitis), endocrine disorders (e.g.

CC acromegaly, thyrotoxicosis), reproductive disorders (gonorrhea,

CC anorchia), gastrointestinal disorders (e.g. gastroenteritis, pyloric

CC stenosis), infectious diseases (e.g. polio, rubella) and cancer.

CC Sequences AB55849-AB558507 represent cDNA molecules encoding human

CC secreted proteins of the invention

XX

SQ Sequence 3798 BP; 1189 A; 749 C; 737 G; 1123 T; 0 U; 0 Other;
Query Match 98.8%; Score 1911.6; DB 6; Length 3798;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1927; Conservative 0; Mismatches 4; Indels 3; Gaps 1;
QY 1 TTGTACCGAAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTCAGAGTCCTAGA 60
DB 310 TTGTACCGAAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTCAGAGTCCTAGA 369
QY 61 TTCCCGAACAGCTACCCCGAGAACCTGCTCTCTGACATGGCGGCTTCACTCTCAGAGAAAT 120
DB 370 TTCCCGAACAGCTACCCCGAGAACCTGCTCTCTGACATGGCGGCTTCACTCTCAGAGAAAT 429
QY 121 ACACGGATACAGCTAGTGTGTTTGACAATCAGTTTCGATTTAGAGGAAGCAAAAATGATATC 180
DB 430 ACACGGATACAGCTAGTGTGTTTGACAATCAGTTTCGATTTAGAGGAAGCAAAAATGATATC 489
QY 181 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCCAGTACCATTTATTAGAGGA 240
DB 490 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCCAGTACCATTTATTAGAGGA 549
QY 241 CGATGGTGTGGACACAAGGAAGTTCTCCCAAGGATAAAATCAAGAACCAAAATTTAAA 300
DB 550 CGATGGTGTGGACACAAGGAAGTTCTCCCAAGGATAAAATCAAGAACCAAAATTTAAA 609
QY 301 ATCACTTCAAGTCCGATGACTACTTTGTGGCTAAAACCTGGATTTCAAGATTTATTATCT 360
DB 610 ATCACTTCAAGTCCGATGACTACTTTGTGGCTAAAACCTGGATTTCAAGATTTATTATCT 669
QY 361 TTGCTGGAAGATTTTCCAAACCGGAGAGCTTCAGAGACCAACTGGGAATCTGTCAACAGC 420
DB 670 TTGCTGGAAGATTTTCCAAACCGGAGAGCTTCAGAGACCAACTGGGAATCTGTCAACAGC 729
QY 421 TCTATTTTCAGGGGTATCCTATACTCTCCATCAGTAAACCGATCCACCTCTGATTCGGAT 480
DB 730 TCTATTTTCAGGGGTATCCTATACTCTCCATCAGTAAACCGATCCACCTCTGATTCGGAT 789
QY 481 GCTCTGGACAAAAAAATTTGCAGAAATTTGATACAGTGGGAAGATCTGCTCAAGTACTTCAAT 540
DB 790 GCTCTGGACAAAAAAATTTGCAGAAATTTGATACAGTGGGAAGATCTGCTCAAGTACTTCAAT 849
QY 541 CCAGATCATGGCAAGAAAGATCTTGAGAAATGATCTGGACACCCCTCGGTATCGAGC 600
DB 850 CCAGATCATGGCAAGAAAGATCTTGAGAAATGATCTGGACACCCCTCGGTATCGAGC 909
QY 601 AGGTCATACCATGACCGGAAGTCAAAAGTTTCACTCGGATAGGCTCAATGATGATGCCAAG 660
DB 910 AGGTCATACCATGACCGGAAGTCAAAAGTTTCACTCGGATAGGCTCAATGATGATGCCAAG 969
QY 661 CGTTACAGTTGCACTCCCGAGAAATTTACTCGGTCAATATAAGAGAAAGCTGAAGTTGCC 720
DB 970 CGTTACAGTTGCACTCCCGAGAAATTTACTCGGTCAATATAAGAGAAAGCTGAAGTTGCC 1029
QY 721 AATGTGCTCTTTTCCACGTTGCTCTCTGTCAGCGCTGTGGAGGAAATTTGGCTGT 780
DB 1030 AATGTGCTCTTTTCCACGTTGCTCTCTGTCAGCGCTGTGGAGGAAATTTGGCTGT 1089
QY 781 GGAATGTCTCACTCGAGGCTCTGCACATGCAATTTCAAGGAAAAACCGTCAAAAAGTATCAT 840
DB 1090 GGAATGTCTCACTCGAGGCTCTGCACATGCAATTTCAAGGAAAAACCGTCAAAAAGTATCAT 1149
QY 841 GAGGTATTACAGTTTGAGCCTGGCCACATCAAGAGGAGGGGTAGAGCTTAAGACCATGCT 900
DB 1150 GAGGTATTACAGTTTGAGCCTGGCCACATCAAGAGGAGGGGTAGAGCTTAAGACCATGCT 1209
QY 901 CTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTTGATCTGCGAGCTCAGAGCA 960
DB 1210 CTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTTGATCTGCGAGCTCAGAGCA 1269
QY 961 CCTCGATAAGAGAATGTGCACATCCTTACATTTAAGCCCTGAAGAACCTTTAGTTAAGGA 1020
DB 1270 CCTCGATAAGAGAATGTGCACATCCTTACATTTAAGCCCTGAAGAACCTTTAGTTAAGGA 1329

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QY 1021 GGTTGAGATAGAGACCCCTTTCTCCTACGACCAACCAAACTTACTACTAGCTGCTCAATGCA 1080
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QY 1081 ATGAAACAAGTGGTCTGCTGAGTCTGAGCTTCCCTGCTGCTTTGTTAAATGCCAATGCCAAGTAGAAA 1140
DB 1390 ATGAAACAAGTGGTCTGCTGAGTCTGAGCTTCCCTGCTGCTTTGTTAAATGCCAATGCCAAGTAGAAA 1449
QY 1141 GGTATATCATCACTCTTATACCTTAAGAATATAGGATGCTATTAATATAGTGGTTGAG 1200
DB 1450 GGTATATCATCACTCTTATACCTTAAGAATATAGGATGCTATTAATATAGTGGTTGAG 1509
QY 1201 GTTATATATGACAAAACACACACAGAAAATATATTCATGCTCTATGCTATATAGATCAAAAT 1260
DB 1510 GTTATATATGACAAAACACACACAGAAAATATATTCATGCTCTATGCTATATAGATCAAAAT 1569
QY 1261 GTTTTTTTGGTATATATACAGGTTACACAGAGCTTACATATGTTTGGTGTAGACTCT 1320
DB 1570 GTTTTTTTGGTATATATACAGGTTACACAGAGCTTACATATGTTTGGTGTAGACTCT 1629
QY 1321 TAAATCTCTTGGCAAAATGAAGGATGGTCAAAATATATGAACATGCTCTTTAGAAAATTT 1380
DB 1630 TAAATCTCTTGGCAAAATGAAGGATGGTCAAAATATATGAACATGCTCTTTAGAAAATTT 1689
QY 1381 AGGAGATAAATTTATTTTAAATTTTGAACACAAAACAAATTTTGAATCTTCTCTCTTA 1440
DB 1690 AGGAGATAAATTTATTTTAAATTTTGAACACAAAACAAATTTTGAATCTTCTCTCTTA 1749
QY 1441 AAGAAAGCATCTGTATATATAAATAAATAAAGATGAGGCTTCTTACATATACATCTTAG 1500
DB 1750 AAGAAAGCATCTGTATATATAAATAAATAAAGATGAGGCTTCTTACATATACATCTTAG 1809
QY 1501 TTGATTTATTAATAAAGGAAAAA---GGTTTCCAGAGAAAAGGCCATACCTTAAGCATTTT 1557
DB 1810 TTGATTTATTAATAAAGGAAAAATATGGTTTCCAGAGAAAAGGCCATACCTTAAGCATTTT 1869
QY 1558 TTCCATGAGAGCACTGCACTACTTACTATGTGACTGTAATAACCTGCTCCAAAACCA 1617
DB 1870 TTCCATGAGAGCACTGCACTACTTACTATGTGACTGTAATAACCTGCTCCAAAACCA 1929
QY 1618 TGCATAATAATATAGTCTTGTAGAAATTAATCAATGCTGTTTTTATGCAATTTGCTG 1677
DB 1930 TGCATAATAATATAGTCTTGTAGAAATTAATCAATGCTGTTTTTATGCAATTTGCTG 1989
QY 1678 AGGCATCTTTATTTCACTTAACACCTATCTCAAAAACCTTACTAGAGGTTTTTTTATATA 1737
DB 1990 AGGCATCTTTATTTCACTTAACACCTATCTCAAAAACCTTACTAGAGGTTTTTTTATATA 2049
QY 1738 GTCCTACAAAAGCAATGATAGCTGTAAACAGAAATTTTGAATGTTTTTCTTTGCAAAA 1797
DB 2050 GTCCTACAAAAGCAATGATAGCTGTAAACAGAAATTTTGAATGTTTTTCTTTGCAAAA 2109
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DB 2110 CCCTCCCAAAAGCAAAATCCCTTCAAGATGCGATGGCATCTGTATGACCTTTTCCA 2169
QY 1858 GATGGTGTTCAGTGAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAACATTTGAACATC 1917
DB 2170 GATGGTGTTCAGTGAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAACATTTGAACATC 2229
QY 1918 GACGTAACCTGGAAA 1931
DB 2230 GACGTAACCTGGAAA 2243
```

RESULT 10
AAD25489
ID AAD25489 standard; DNA; 3718 BP.
XX
AC AAD25489;
XX
DT 26-MAR-2002 (first entry)

Human LP85 DNA #2.
LP85; platelet-derived growth factor; PDGF; antiinflammatory; vulnerary;
osteopathic; neuroprotective; tranquiliser; musculoskeletal disorder;
MSD; therapy; bone growth; cartilage differentiation; wound healing;
neuron growth; bone fracture; osteoporosis; osteopenia; arthritis;
sarcopenia; periodontal disease; tissue atrophy; endocrine disorder;
muscle loss; immobility; bone density; ds.
Homo sapiens.
Key Location/Qualifiers
CDS 114..1208
/tag= a
/product= "Human LP85 protein"
FT sig_peptide 114..149
/tag= b
FT mat_peptide 150..1205
/tag= c
/product= "Human mature LP85 protein"
WO200189450-A2.
29-NOV-2001.
08-MAY-2001; 2001WO-US011755.
19-MAY-2000; 2000US-0205424P.
11-JAN-2001; 2001US-0261071P.
11-JAN-2001; 2001US-0261076P.
(ELIL) LILLY & CO ELI.
Beals JM, Gonzalez-Dewhitt PA, Hammond LJ, Lu J, Na S, Su EW;
Witcher DR, Wroblewski VJ;
WPI; 2002-083040/11.
P-PSDB; AAE15820.
Analog of a platelet-derived growth factor homolog, LP85 useful for
treating osteoporosis, arthritis, sarcopenia, wounds, has one or more
amino acid substitutions which destroy the tripeptidyl sequence of native
LP85.
Disclosure; Page 111-113; 117pp; English.
The present invention relates to LP85, an analogue of platelet-derived
growth factor (PDGF) homologue. Sequences of the invention are useful for
the manufacture of a medicament for treating musculoskeletal disorder
(MSD) which include promoting bone growth, cartilage differentiation and
function, wound healing, neuron growth, preventing cartilage degradation
or neuronal degeneration. They are useful for treating bone fractures,
osteoporosis, osteopenia, arthritis, sarcopenia, periodontal disease,
tissue atrophy, traumatised connective tissues, grafted connective
tissues and/or transplanted organs, bone or muscle loss due to
malignancy, endocrine disorders and immobility. They are also used for
prophylactically increasing or maintaining bone density in a mammal. The
present sequence is a DNA encoding human LP85 protein
Sequence 3718 BP; 1157 A; 730 C; 715 G; 1116 T; 0 U; 0 Other;

Query Match 98.4%; Score 1903.6; DB 6; Length 3718;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1922; Conservative 0; Mismatches 9; Indels 3; Gaps 1;
QY 1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACCGGTACGTCGACAGTCCTAGA 60
DB 240 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACCGGTACGTCGACAGTCCTAGA 299
QY 61 TTCCCGAACAGCTACCCCGAGAACCTGCTCTGACATGGCGGCTTCACTCTCAGGAGAAAT 120
DB 300 TTCCCGAACAGCTACCCCGAGAACCTGCTCTGACATGGCGGCTTCACTCTCAGGAGAAAT 359

QY	121	ACCGGATACAGCTAGTGTGTCACATCAGCTTTGGATTAGAGGAAGCGAAAAATGATATC	180
DB	360	ACCGGATACAGCTAGTGTGTCACATCAGCTTTGGATTAGAGGAAGCGAAAAATGATATC	419
QY	181	TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCCAGTACCATTATTAGAGGA	240
DB	420	TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCCAGTACCATTATTAGAGGA	479
QY	241	CGATGGTGGACACAAGAAAGTTCTCCAAAGGATAAAATCAAGAACGAAACCAAAATTA	300
DB	480	CGATGGTGGACACAAGAAAGTTCTCCAAAGGATAAAATCAAGAACGAAACCAAAATTA	539
QY	301	ATCACATTCAAGTCGGATGACTATTTGTGGCTAAACCTGGATTCAAGATTATTATCT	360
DB	540	ATCACATTCAAGTCGGATGACTATTTGTGGCTAAACCTGGATTCAAGATTATTATCT	599
QY	361	TTGCTGGAAGATTTCACACCGCAGCAGCTTCAGAGACCAACTGGGAATCTGCACAGC	420
DB	600	TTGCTGGAAGATTTCACACCGCAGCAGCTTCAGAGACCAACTGGGAATCTGCACAGC	659
QY	421	TCTATTTCCAGGGTATCCTATAACTCTCCATCAGTAAACGGATCCCACTCTGATTGCGGAT	480
DB	660	TCTATTTCCAGGGTATCCTATAACTCTCCATCAGTAAACGGATCCCACTCTGATTGCGGAT	719
QY	481	GCTCTGGACAAAAAATTTGCGAATTTGATACAGTGGGAAGATCTGCTCAAGTACTTCAAT	540
DB	720	GCTCTGGACAAAAAATTTGCGAATTTGATACAGTGGGAAGATCTGCTCAAGTACTTCAAT	779
QY	541	CCAGAGTCATCGCAGAGAGATCTTGAGAAATATGATCTGGACACCCCTCGGTATCGAGGC	600
DB	780	CCAGAGTCATCGCAGAGAGATCTTGAGAAATATGATCTGGACACCCCTCGGTATCGAGGC	839
QY	601	AGGTCATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG	660
DB	840	AGGTCATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG	899
QY	661	CGTTACAGTTGACCTCCAGGAATTAATCTCGGTCAATATAAGAGAGAGCTGAAGTTGGCC	720
DB	900	CGTTACAGTTGACCTCCAGGAATTAATCTCGGTCAATATAAGAGAGAGCTGAAGTTGGCC	959
QY	721	AATGTGGTCTCTTCCAGCTTGCTCTCTGTCGAGCGCTGTGGAGGAATTTGGCTGT	780
DB	960	AATGTGGTCTCTTCCAGCTTGCTCTCTGTCGAGCGCTGTGGAGGAATTTGGCTGT	1019
QY	781	GGAACTGTCAACTGGAGTCTCTGCACATGCAATTCAGGGAACCCGTCGAAAAAGTATCAT	840
DB	1020	GGAACTGTCAACTGGAGTCTCTGCACATGCAATTCAGGGAACCCGTCGAAAAAGTATCAT	1079
QY	841	GAGGTATTACAGTTTGACCTGGCCACATCAAGAGAGGGGTAGAGCTAAGACCATGGCT	900
DB	1080	GAGGTATTACAGTTTGACCTGGCCACATCAAGAGAGGGGTAGAGCTAAGACCATGGCT	1139
QY	901	CTAGTTGACATCCAGTTGGATCACCATCAAGATGCGATTGTTATCTGCAGCTCAAGACCA	960
DB	1140	CTAGTTGACATCCAGTTGGATCACCATCAAGATGCGATTGTTATCTGCAGCTCAAGACCA	1199
QY	961	CCTCGATAAGAGAATGTGCATCTTACATTAAGCTCGAAAGAACCTTTAGTTTAAAGGA	1020
DB	1200	CCTCGATAAGAGAATGTGCATCTTACATTAAGCTCGAAAGAACCTTTAGTTTAAAGGA	1259
QY	1021	GGGTGAGATAAGAGACCTTTTCTTACCAGCAACCAAACTTACTACTAGCTGCAATGCA	1080
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QY	1081	ATGAACACAAGTGGTGTGAGTCTCAGCTTGTCTTGTAAATGCGCATGGCAAGTAGAAA	1140
DB	1320	ATGAACACAAGTGGTGTGAGTCTCAGCTTGTCTTGTAAATGCGCATGGCAAGTAGAAA	1379
QY	1141	GGTATATCATCAACTTCTATACCTAAGAAATATAGGATTGCAATTAATATAGTGTTCAG	1200
DB	1380	GGTATATCATCAACTTCTATACCTAAGAAATATAGGATTGCAATTAATATAGTGTTCAG	1439

QY	1201	GTTATATATGCACAAACACACACAGAAATATATTATCTATCTATGTATATAGATCAAAAT	1260
DB	1440	GTTATATATGCACAAACACACACAGAAATATATTATCTATCTATGTATATAGATCAAAAT	1499
QY	1261	GTTTTTTTTTGGTATATATAACAGGTACACACAGAGCTTACATATGTTTGGTTAGACTCT	1320
DB	1500	GTTTTTTTTTGGTATATATAACAGGTACACACAGAGCTTACATATGTTTGGTTAGACTCT	1559
QY	1321	TAAATCTTTTGGCCAAAATTAAGGATGGTCAAATATATGAAAAATGTTTGAATAATTT	1380
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QY	1381	AGGAGATAAATTTTAAATTTTGAACACACAAACAAATTTTGAATCTTTGCTCTCTTA	1440
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QY	1441	AAGAAAGCATCTCTGTATATTAATAATCAAAAGATGAGGCTTTCTTACATATACATCTTAG	1500
DB	1680	AAGAAAGCATCTCTGTATATTAATAATCAAAAGATGAGGCTTTCTTACATATACATCTTAG	1739
QY	1501	TTGATTTATTAATAAGGAAAAA---GGTTTCCAGAGAAAAAGGCCAAATACCTTAAGCATTTT	1557
DB	1740	TTGATTTATTAATAAGGAAAAAATATGGTTTCCAGAGAAAAAGGCCAAATACCTTAAGCATTTT	1799
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DB	1800	TTCCATCAGAGACACTGCATCTTACCTATGCTGACCTGTAATACCTGCTCTCCAAACCA	1859
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DB	1860	TGCCATTAATAATAAGTGGCTTTAGAAAATTAATAATCATTTGTTTTTATGCAATTTTGGTG	1919
QY	1678	AGGCATCTTTATTCATTTAACACCTATCTCAAAAACTTACTTAGAAGGTTTTTTATTATA	1737
DB	1920	AGGCATCTTTATTCATTTAACACCTATCTCAAAAACTTACTTAGAAGGTTTTTTATTATA	1797
QY	1738	GTCCTACAAAAGACAAATGTATAAGCTGTACACAGAAATTTGAAATGTTTTTCTTGGCAAA	1797
DB	1980	GTCCTACAAAAGACAAATGTATAAGCTGTACACAGAAATTTGAAATGTTTTTCTTGGCAAA	2039
QY	1798	CCCCTCACAAAAGCAAAATCCTTTCAAGAAATGGCATGGCAATCTGTATGAACCTTTCCA	1857
DB	2040	CCCCTCACAAAAGCAAAATCCTTTCAAGAAATGGCATGGCAATCTGTATGAACCTTTCCA	2099
QY	1858	GATGGTGTTCAGTGAAGAAGATGGGTAGTTGAGAACTTAAAAAGTGAACATTGAAACATC	1917
DB	2100	GATGGTGTTCAGTGAAGAAGATGGGTAGTTGAGAACTTAAAAAGTGAACATTGAAACATC	2159
QY	1918	GACGTAACCTGGAAA 1931	
DB	2160	GACGTAACCTGGAA 2173	
RESULT 11			
ID	AAD25488 standard; DNA; 3736 BP.		
AC	AAD25488;		
DT	26-MAR-2002 (first entry)		
DE	Human LP85 DNA #1.		
KW	LP85; platelet-derived growth factor; PDGF; antiinflammatory; vulnery;		
KW	osteopathic; neuroprotective; tranquilliser; musculoskeletal disorder;		
KW	MSD; therapy; bone growth; cartilage differentiation; wound healing;		
KW	neuron growth; bone fracture; osteoporosis; osteopenia; arthritis;		
KW	sarcopenia; periodontal disease; tissue atrophy; endocrine disorder;		
OS	muscle loss; immobility; bone density; ds.		
XX	Homo sapiens.		
FH	Key	Location/Qualifiers	

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 /product= "Human mature LP85 protein"
 WO200189450-A2.
 29-NOV-2001.
 08-MAY-2001; 2001WO-US011755.
 19-MAY-2000; 2000US-0205424P.
 11-JAN-2001; 2001US-0261071P.
 11-JAN-2001; 2001US-0261076P.
 (ELIL) LILLY & CO ELI.
 Beals JM, Gonzalez-Dewhitt PA, Hammond LJ, Lu J, Na S, Su EW;
 Witcher DR, Wroblewski VJ;
 WPI; 2002-083040/11.
 P-PSDB; AAE15819.
 Analog of a platelet-derived growth factor homolog, LP85 useful for
 treating osteoporosis, arthritis, sarcopenia, wounds, has one or more
 amino acid substitutions which destroy the tripeptidyl sequence of native
 LP85.
 Disclosure; Page 106-109; 117pp; English.
 The present invention relates to LP85, an analogue of platelet-derived
 growth factor (PDGF) homologue. Sequences of the invention are useful for
 the manufacture of a medicament for treating musculoskeletal disorder
 (MSD) which include promoting bone growth, cartilage differentiation and
 function, wound healing, neuron growth, preventing cartilage degradation
 or neuronal degeneration. They are useful for treating bone fractures,
 osteoporosis, sarcopenia, arthritis, sarcopenia, periodontal disease,
 tissue atrophy, traumatised connective tissues, grafted connective
 tissues and/or transplanted organs, bone or muscle loss due to
 malignancy, endocrine disorders and immobility. They are also used for
 prophylactically increasing or maintaining bone density in a mammal. The
 present sequence is a DNA encoding human LP85 protein
 Sequence 3736 BP; 1164 A; 736 C; 718 G; 1118 T; 0 U; 0 Other;

Query Match 98.4%; Score 1903.6; DB 6; Length 3736;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 1922; Conservative 0; Mismatches 9; Indels 3; Gaps 1;

QY 1 TTGTACCGAAGATGAGACCATCCAGGTGAAGGAACGGCTAGTCGAGAGTCTTACA 60
 DB 258 TTGTACCGAAGATGAGACCATCCAGGTGAAGGAACGGCTAGTCGAGAGTCTTACA 317
 QY 61 TTCCCGAACAGCTACCCAGGAACCTGCTCTGACATGGCGGCTTCACTCTCAGGAGAT 120
 DB 318 TTCCCGAACAGCTACCCAGGAACCTGCTCTGACATGGCGGCTTCACTCTCAGGAGAT 377
 QY 121 ACACGGATACAGTGTGTTGACAAATCAGTTGGATTAGAGGAACGAAATGATATC 180
 DB 378 ACACGGATACAGTGTGTTGACAAATCAGTTGGATTAGAGGAACGAAATGATATC 437
 QY 181 TGTAGTATGTTTGTGGAAGTTGAAGATATATCCGAAACAGTACCATTATTAGAGGA 240
 DB 438 TGTAGTATGTTTGTGGAAGTTGAAGATATATCCGAAACAGTACCATTATTAGAGGA 497
 QY 241 CGATGGTGGACACAAGGAAGTCTCTCCAGGATAAAATCAAGAACGAACCAATTTAA 300
 DB 498 CGATGGTGGACACAAGGAAGTCTCTCCAGGATAAAATCAAGAACGAACCAATTTAA 557

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 QY 618 TTGCTGGAAGATTTCCAAACCCGACAGCAGCTTTCAGAGACCAACTGGGAATCTGTCAAGC 677
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 DB |||||
 QY 678 TCTATTTGAGGGTATCCTATAAATCTCTCATCAGTAACGGATCCCACTGTGATTCGGAT 737
 DB |||||
 QY 481 GCTCTGGACAAAAAATTCAGAAATTCATACAGTGGAAAGATCTGCTCAAGTACTTCAAT 540
 DB |||||
 QY 738 GCTCTGGACAAAAAATTCAGAAATTCATACAGTGGAAAGATCTGCTCAAGTACTTCAAT 797
 DB |||||
 QY 541 CCAGAGTCATGCGAAGAAGATCTTTGAGAATATGTATCTGGACACCCCTCGGTATCGAGGC 600
 DB |||||
 QY 798 CCAGAGTCATGCGAAGAAGATCTTTGAGAATATGTATCTGGACACCCCTCGGTATCGAGGC 857
 DB |||||
 QY 601 AGGTCATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
 DB |||||
 QY 858 AGGTCATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 917
 DB |||||
 QY 661 CGTTACAGTTGCACCTCCAGGAATTTACTCGGTCAATATAAGAGAAAGAGCTGAAGTTGCC 720
 DB |||||
 QY 918 CGTTACAGTTGCACCTCCAGGAATTTACTCGGTCAATATAAGAGAAAGAGCTGAAGTTGCC 977
 DB |||||
 QY 721 AATGTGTTCTTTTCCAGTTGGCTCTCTCGAGCGCTGTGGAGGAAATGTGGTGT 780
 DB |||||
 QY 978 AATGTGTTCTTTTCCAGTTGGCTCTCTCGAGCGCTGTGGAGGAAATGTGGTGT 1037
 DB |||||
 QY 781 GGAATGTCACCTGAGGTCTCGACATGCAATTTGAGGAAACCGTGAAAGATATCAT 840
 DB |||||
 QY 1038 GGAATGTCACCTGAGGTCTCGACATGCAATTTGAGGAAACCGTGAAAGATATCAT 1097
 DB |||||
 QY 841 GAGGTATTACAGTTTGGAGCTGGCCACATCAAGAGAGGGGTAGAGCTAAGACCATGGCT 900
 DB |||||
 QY 1098 GAGGTATTACAGTTTGGAGCTGGCCACATCAAGAGAGGGGTAGAGCTAAGACCATGGCT 1157
 DB |||||
 QY 901 CTAGTTGACATCCAGTTGGATCACCATGAAGAGCGATTTGTATCTGCGAGCTCAAGACCA 960
 DB |||||
 QY 1158 CTAGTTGACATCCAGTTGGATCACCATGAAGAGCGATTTGTATCTGCGAGCTCAAGACCA 1217
 DB |||||
 QY 961 CCTCGATAAGAGAATGTGCACATCCTTTACATTAAGCTGAAAGAACCTTTAGTTTAAAGGA 1020
 DB |||||
 QY 1218 CCTCGATAAGAGAATGTGCACATCCTTTACATTAAGCTGAAAGAACCTTTAGTTTAAAGGA 1277
 DB |||||
 QY 1021 GGGTGAGATAAGAGACCCCTTTTCTACAGCAACCAAACTTACTACTAGCTGCAATGCA 1080
 DB |||||
 QY 1278 GGGTGAGATAAGAGACCCCTTTTCTACAGCAACCAAACTTACTACTAGCTGCAATGCA 1337
 DB |||||
 QY 1081 ATGAACACAGTGGTGTGAGTCTGAGCTTGTGTTTGTAAATGCCATGCCAAGTAGAAA 1140
 DB |||||
 QY 1338 ATGAACACAGTGGTGTGAGTCTGAGCTTGTGTTTGTAAATGCCATGCCAAGTAGAAA 1397
 DB |||||
 QY 1141 GGTATATCATCAACTTCTATACCTTAAGAATATAGGATTTGATTAATAAGTGTGTTGAG 1200
 DB |||||
 QY 1398 GGTATATCATCAACTTCTATACCTTAAGAATATAGGATTTGATTAATAAGTGTGTTGAG 1457
 DB |||||
 QY 1201 GTTATATATGCAAAACACACACAGAAATATATTTGATGTGTATATAGATCAAAAT 1260
 DB |||||
 QY 1458 GTTATATATGCAAAACACACACAGAAATATATTTGATGTGTATATAGATCAAAAT 1517
 DB |||||
 QY 1261 GTTTTTTTTGTATATATACCGAGTACACAGAGCTTACATATGTTGAGTTAGACTCT 1320
 DB |||||
 QY 1518 GTTTTTTTTGTATATATACCGAGTACACAGAGCTTACATATGTTGAGTTAGACTCT 1577
 DB |||||
 QY 1321 TAAATCCTTTTGCAGAAATTAAGGATGCTCAAAATATATATGAAACATGCTTTTAAAGAAATTT 1380
 DB |||||
 QY 1578 TAAATCCTTTTGCAGAAATTAAGGATGCTCAAAATATATATGAAACATGCTTTTAAAGAAATTT 1637
 DB |||||
 QY 1381 AGGAGTAAATTTATTTTAAATTTTGAACACAAACAAATTTTGAATCTTCTCTCTTA 1440

QY 781 GGAACTGTCACTGGAGTCTTGCAATGCAATTCAGGAAACCGTGAAAAAGTATCAT 840
Db |||||
QY 1137 CGAACTGTCACTGGAGTCTTGCAATGCAATTCAGGAAACCGTGAAAAAGTATCAT 1196
Db |||||
QY 841 GAGGTATTACAGTTTGGAGTCTGGCCACATCAAGAGAGGGGTAGAGCTTAAGACCATGGCT 900
Db |||||
QY 1197 GAGGTATTACAGTTTGGAGTCTGGCCACATCAAGAGAGGGGTAGAGCTTAAGACCATGGCT 1256
Db |||||
QY 901 CTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTGTATCTGCAGCTCAAGACCA 960
Db |||||
QY 1257 CTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTGTATCTGCAGCTCAAGACCA 1316
Db |||||
QY 961 CTTGATTAAGAAATGTGACATCTTACATTAAGCTTGAAGAAACCTTTAGTTTAAAGGA 1020
Db |||||
QY 1317 CTTGATTAAGAAATGTGACATCTTACATTAAGCTTGAAGAAACCTTTAGTTTAAAGGA 1376
Db |||||
QY 1021 GGGTGAGATAAGAGACCCCTTTTCTACAGCAACCAAACTTACTACTAGCCCTGCAATGCA 1080
Db |||||
QY 1377 GGGTGAGATAAGAGACCCCTTTTCTACAGCAACCAAACTTACTACTAGCCCTGCAATGCA 1436
Db |||||
QY 1081 ATGAACACAAGTGGTGTGCTGAGTCTCAGCCTTGTCTTGTATGTCATGGCAAGTAGAAA 1140
Db |||||
QY 1437 ATGAACACAAGTGGTGTGCTGAGTCTCAGCCTTGTCTTGTATGTCATGGCAAGTAGAAA 1496
Db |||||
QY 1141 GGTATATCATCAACTTCTATACCTAAGAAATAGAGTTGCATTTAATAATAGTTTTCAG 1200
Db |||||
QY 1497 GGTATATCATCAACTTCTATACCTAAGAAATAGAGTTGCATTTAATAATAGTTTTCAG 1556
Db |||||
QY 1201 GTTATATATGCAACAACACACACAGAAATATATTCATCTATGTATATAGATCAAAAT 1260
Db |||||
QY 1557 GTTATATATGCAACAACACACAGAAATATATTCATCTATGTATATAGATCAAAAT 1616
Db |||||
QY 1261 G--TTTTTTTGGTATATATAACACAGGTACACAGAGCTTACATATGTTTGGAGTTAGACT 1318
Db |||||
QY 1617 GTTTTTTTTGGTATATATAACACAGGTACACAGAGTTACATATGTTTGGAGTTAGACT 1676
Db |||||
QY 1319 CTTAAATATCTTTGGCAAAATGAAGGATGGTCAAAATATATGAAACATGCTTTTGAAGAAAT 1378
Db |||||
QY 1677 CTTAAATATCTTTGGCAAAATGAAGGATGGTCAAAATATATGAAACATGCTTTTGAAGAAAT 1736
Db |||||
QY 1379 TTAGGAGATAAATTTATTTTAAATTTTGAACACAAACAAATTTTGAATCTTGTCTCTCT 1438
Db |||||
QY 1737 TTAGGAGATAAATTTATTTTAAATTTTGAACACGAAACAAATTTTGAATCTTGTCTCTCT 1796
Db |||||
QY 1439 TAAAGAAAGCATCTTGTATATATAAATAACAAAGATGAGGCTTCTTACATATACATCTT 1498
Db |||||
QY 1797 TAAAGAAAGCATCTTGTATATATAAATAACAAAGATGAGGCTTCTTACATATACATCTT 1856
Db |||||
QY 1499 AGTTGATTTAATAAAGGAAAA--GGTTTCCAGAGAAAGGCAATACCTAAGCAAT 1555
Db |||||
QY 1857 AGTTGATTTAATAAAGGAAAAATATGTTTCCAGAGAAAGGCAATACCTAAGCAAT 1916
Db |||||
QY 1556 TTTTCCATGAGAGCACTGCATCTTACCTATGTGAGCTGTAATACCTGCTCCCAAAAC 1615
Db |||||
QY 1917 TTTTCCATGAGAGCACTGCATCTTACCTATGTGAGCTGTAATACCTGCTCCCAAAAC 1976
Db |||||
QY 1616 CATGCCATAATATAAGTGTCTTTAGAAATTAATCATTTGTGTTTTTATGCAATTTTGC 1675
Db |||||
QY 1977 CATGCCATAATATAAGTGTCTTTAGAAATTAATCATTTGTGTTTTTATGCAATTTTGC 2036
Db |||||
QY 1676 TGAGGATCTTATTTATTAACCTATCTCAAAAACCTTACTTAGAGAGGTTTTTATTA 1735
Db |||||
QY 2037 TGAGGATCTTATTTATTTATTAACCTATCTCAAAAACCTTACTTAGAGAGGTTTTTATTA 2096
Db |||||
QY 1736 TAGTCTCAAAAAGCAATGTATAGCTGTACAGAAATTTTGAATTTTCTTTGCA 1795
Db |||||
QY 2097 TAGTCTCAAAAAGCAATGTATAGCTGTACAGAAATTTTGAATTTTCTTTGCA 2156
Db |||||
QY 1796 AACCCCTCCAAAAAGCAAAATCTTTCAAGATGGCATGGGCAATCTCTATGAACCTTTTC 1855
Db |||||
QY 2157 AACCCCTCCAAAAAGCAAAATCTTTCAAGATGGCATGGGCAATCTCTATGAACCTTTTC 2216
Db |||||
QY 1856 CAGATGGTGTTCAGTGAAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAACATTGAACA 1915

Db 2217 CAGATGGTGTTCAGTGAAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAACATTGAACA 2276
QY 1916 TCGACGTAACCTGGAAA 1931
Db 2277 TCGACGTAACCTGGAAA 2292
RESULT 13
ADQ23870
ID ADQ23870 standard; DNA; 4153 BP.
XX
AC ADQ23870;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6690.
XX
KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
XX ds.
XX Homo sapiens.
XX OS
XX PN WO2004048938-A2.
XX PD 10-JUN-2004.
XX PF 26-NOV-2003; 2003WO-US038193.
XX PR 26-NOV-2002; 2002US-0429739P.
XX PA (PROT-) PROTEIN DESIGN LABS INC.
XX PI Aziz N, Ginsburg WM, Zlotnik A;
XX DR WPI; 2004-441208/41.
XX
PT Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX
PS Example 2; SEQ ID NO 6690; 210pp; English.
XX
CC The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytosstatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC DNA of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX
SQ Sequence 4153 BP; 1253 A; 855 C; 854 G; 1174 T; 0 U; 17 Other;
Query Match 98.0%; Score 1896.2; DB 12; Length 4153;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1911; Conservative 0; Mismatches 20; Indels 3; Gaps 1;
QY 1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAGAAACGGCTACGTGCAGAGTCCTAGA 60
Db |||||
QY 602 TTGTACCGAAGAGATGAGACCATCCAGTGAAGAAACGGCTACGTGCAGAGTCCTAGA 661
Db |||||
QY 61 TTCCGGAACAGCTACCCCGAGGAACCTGCTCTCTGACATGGCGGCTTCACTCTCAGGAGAAT 120
Db |||||
QY 662 TTCCGGAACAGCTACCCCGAGGAACCTGCTCTCTGACATGGCGGCTTCACTCTCAGGAGAAT 721
Db |||||
QY 121 ACAGGATACAGCTAGTGTGTTGACATCAGTTTGGATTAGAGGAACGAGAAATGATATC 180

Db 722 AC CGGATACAGCTAGTGTGTTGCAATCAGTTTGGATTAGAGGAAGCAGAAAATGATATC 781
Qy 181 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCAAGTACCATTTATTAGAGGA 240
Db 782 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCAAGTACCATTTATTAGAGGA 841
Qy 241 CGATGGTGTGGACACAAGGAAGTTCTCCCAAGGATATAAATCAAGAACGAACCAAAATTA 300
Db 842 CGATGGTGTGGACACAAGGAAGTTCTCCCAAGGATATAAATCAAGAACGAACCAAAATTA 901
Qy 301 ATCAATTCAGATCCGATGACTACTTGTGTGCTAAACCTGGATCAAGATTTATTATTCT 360
Db 902 ATCAATTCAGATCCGATGACTACTTGTGTGCTAAACCTGGATCAAGATTTATTATTCT 961
Qy 361 TTGCTGGAAGATTTCCAAACCGCAGCAGCTTCAGAGACCAACTGGGAATCTGTCCACAAGC 420
Db 962 TTGCTGGAAGATTTCCAAACCGCAGCAGCTTCAGAGACCAACTGGGAATCTGTCCACAAGC 1021
Qy 421 TCTATTTTCAGGGTATCTTATACTTCCATCAGTAACGGATCCCACTCTGATTTGGCGAT 480
Db 1022 TCTATTTTCAGGGTATCTTATACTTCCATCAGTAACGGATCCCACTCTGATTTGGCGAT 1081
Qy 481 GCTCTGACAAAAAATTTGCAAGATTTGCATACAGTGGGAAGATCTGCTCAAGTACTTCAAT 540
Db 1082 GCTCTGACAAAAAATTTGCAAGATTTGCATACAGTGGGAAGATCTGCTCAAGTACTTCAAT 1141
Qy 541 CCAGAGTCATGGCAAGAAGATCTTGGAGAAATGTATCTGGACACCCCTCGGTATCGAGGC 600
Db 1142 CCAGAGTCATGGCAAGAAGATCTTGGAGAAATGTATCTGGACACCCCTCGGTATCGAGGC 1201
Qy 601 AGGTCATACCAATCCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
Db 1202 AGGTCATACCAATCCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 1261
Qy 661 GGTTCAGTTGCATCCGAGAAATTAATCTCGTCAATATAAGAGAGAGCTGAAGTTGGCC 720
Db 1262 GGTTCAGTTGCATCCGAGAAATTAATCTCGTCAATATAAGAGAGAGCTGAAGTTGGCC 1321
Qy 721 AATGTGTTCTTTTCCAGTTGCTCTCTCGTGCAGCGCTGTGGAGGAAATTTGTGGCTGT 780
Db 1322 AATGTGTTCTTTTCCAGTTGCTCTCTCGTGCAGCGCTGTGGAGGAAATTTGTGGCTGT 1381
Qy 781 GGAATCTGCAATCGAGGTCTGCAATGCAATTCAGGGAACCGTGAAGAAATGATCAT 840
Db 1382 GGAATCTGCAATCGAGGTCTGCAATGCAATTCAGGGAACCGTGAAGAAATGATCAT 1441
Qy 841 GAGGTATTACAGTTTGAGCTGGCCACATCAAGAGGGGTAGAGCTAAGACCATGCT 900
Db 1442 GAGGTATTACAGTTTGAGCTGGCCACATCAAGAGGGGTAGAGCTAAGACCATGCT 1501
Qy 901 CTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTTGATCTGCAGCTCAAGACCA 960
Db 1502 CTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTTGATCTGCAGCTCAAGACCA 1561
Qy 961 CCTCGATAAGAGAATGTGCAATCTTACATTAAGCTGGAAGAACCTTTAGTTAAGGA 1020
Db 1562 CCTCGATAAGAGAATGTGCAATCTTACATTAAGCTGGAAGAACCTTTAGTTAAGGA 1621
Qy 1021 GGGTGAGATAAGAGACCTTTTCTTACCAGCAACCAAACTTACTAGCTGCAATGCA 1080
Db 1622 GGGTGAGATAAGAGACCTTTTCTTACCAGCAACCAAACTTACTAGCTGCAATGCA 1681
Qy 1081 ATGAACACAAGTTGTTGCTGAGTCTCAGCTTGTCTTGTAAATGCGCATGGCAAGTAGAAA 1140
Db 1682 ATGAACACAAGTTGTTGCTGAGTCTCAGCTTGTCTTGTAAATGCGCATGGCAAGTAGAAA 1741
Qy 1141 GGTATATCATCAACTTCTATACCTAAGAAATATAGGATTTGCAATTAATATAGTTTCAG 1200
Db 1742 GGTATATCATCAACTTCTATACCTAAGAAATATAGGATTTGCAATTAATATAGTTTCAG 1801
Qy 1201 GTTATATATGACAAACACACACAGAAATATATTCTGCTATGTTATATAGATCAAAAT 1260

Db 1802 GTTATATATGACAAACACACACAGAAATATATTCTATGCTCTATGTTATAGATCAAAAT 1861
Qy 1261 GTTTTTTTTGGTATATATAAACCCAGGTACACACAGAGCTTACATATGTTTGGTTAGACTCT 1320
Db 1862 GTTTTTTTTGGTATATATAAACCCAGGTACACACAGAGCTTACATATGTTTGGTTAGACTCT 1921
Qy 1321 TAAATCCTTTGGCCAAATTAAGGATGCTCAAAATATATGAACATGCTCTTTAGAAAAATTT 1380
Db 1922 TAAATCCTTTGGCCAAATTAAGGATGCTCAAAATATATGAACATGCTCTTTAGAAAAATTT 1981
Qy 1381 AGGAGATAAAATTTATTTTAAATTTTGAACACAAAAACAATTTTGAATCTTGTCTCTCTTA 1440
Db 1982 AGGAGATAAAATTTATTTTAAATTTTGAACACAAAAACAATTTTGAATCTTGTCTCTCTTA 2041
Qy 1441 AAGAAACATCTTGTATATTAATAATCAAAAGATGAGGCTTCTTACATATACATCTTAG 1500
Db 2042 AAGAAACATCTTGTATATTAATAATCAAAAGATGAGGCTTCTTACATATACATCTTAG 2101
Qy 1501 TTGATTTATTAATAAGGAAAAA---GGTTTCCAGAGAAAAAGGCCAATACCTTAAGCATTTT 1557
Db 2102 TTGATTTATTAATAAGGAAAAATATGTTTCCAGAGAAAAAGGCCAATACCTTAAGCATTTT 2161
Qy 1558 TTCCATGAGAGACACTGCATACCTTACCTATGTGTGACTGTATAACCTGTCTCCAAAAACA 1617
Db 2162 TTCCATGAGAGACACTGCATACCTTACCTATGTGTGACTGTATAACCTGTCTCCAAAAACA 2221
Qy 1618 TGCCATTAATATAAAGTCTTTAGAAAATTAATAATCATTTGTGTTTTTATGCAATTTTGTCTG 1677
Db 2222 TGCCATTAATATAAAGTCTTTAGAAAATTAATAATCATTTGTGTTTTTATGCAATTTTGTCTG 2281
Qy 1678 AGGCATCCTTTATTTCAATTTAACACCTATCTCAAAAACCTTACTTAGAAGGTTTTTATTATA 1737
Db 2282 AGGCATCCTTTATTTCAATTTAACACCTATCTCAAAAACCTTACTTAGAAGGTTTTTATTATA 2341
Qy 1738 GTCCCTCAAAAGACAAATGTATAAGCTGTAAACAGAAATTTGAATTTGTTTTCTTTGCAAAA 1797
Db 2342 GTCCCTCAAAAGACAAATGTATAAGCTGTAAACAGAAATTTGAATTTGTTTTCTTTGCAAAA 2401
Qy 1798 CCCCTCCACAAAAAGCAAAATCCTTTCAAGAAATGGCAATGGGCATTTCTGTATGAACCTTTTCCA 1857
Db 2402 CCCCTCCACAAAAAGCAAAATCCTTTCAAGAAATGGCAATGGGCATTTCTGTATNNNNNNNNN 2461
Qy 1858 GATGGTCTTCAGTCAAAAGATGCTGGGTAGTTGAGAACTTAAAGAGTGAACATTTGAACATC 1917
Db 2462 NNNNNNGTTTCAAGTCAAAAGATGCTGGGTAGTTGAGAACTTAAAGAGTGAACATTTGAACATC 2521
Qy 1918 GACGTAACTGGAAA 1931
Db 2522 GACGTAACTGGAAA 2535
RESULT 14
ADQ22990
ID ADQ22990 standard; DNA; 4153 BP.
XX ADQ22990;
AC ADQ22990;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5810.
XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
KW ds.
XX Homo sapiens.
OS
XX WO2004048938-A2.
PN
XX 10-JUN-2004.
PD
XX 26-NOV-2003; 2003WO-US038193.
PF
XX 26-NOV-2002; 2002US-0429739P.
PR

XX	(PROT-) PROTEIN DESIGN LABS INC.		
PA	Aziz N, Ginsburg WM, Zlotnik A;		
XX	WPI; 2004-441208/41.		
XX	Early detection of soft tissue sarcoma comprises determining expression		
PT	of a gene in a first soft tissue sample and a normal soft tissue sample		
PT	and comparing the gene expression, also useful in treating soft tissue		
PT	sarcoma.		
XX	Example 2; SEQ ID NO 5810; 210pp; English.		
PS			
XX	The invention relates to a novel method for detecting soft tissue sarcoma		
CC	which comprises obtaining a first soft tissue sample from an individual		
CC	and a normal soft tissue sample from the same or different individual,		
CC	determining the expression of a gene in both samples and comparing the		
CC	expression of the gene in both soft tissue samples, where a higher level		
CC	of protein expression in the first soft tissue sample indicates the		
CC	presence of soft tissue sarcoma. The method of the invention has		
CC	cytostatic applications and may be useful for detecting soft tissue		
CC	sarcoma, possibly via gene therapy or vaccine production. The nucleic		
CC	acid sequences may be useful in diagnostic and screening applications.		
CC	The current sequence is that of a human soft tissue sarcoma-upregulated		
CC	DNA of the invention. The current sequence is not shown within the		
CC	specification per se but was submitted in CD format by the inventor.		
XX	Sequence 4153 BP; 1253 A; 855 C; 854 G; 1174 T; 0 U; 17 Other;		
SQ			
Query Match 98.0%; Score 1896.2; DB 12; Length 4153;			
Best Local Similarity 98.8%; Pred. No. 0;			
Matches 1911; Conservative 0; Mismatches 20; Indels 3; Gaps 1;			
QY	1 TTGTACCGAAGATGAGACCATCCAGGTGAAGGAAACGGCTAGTCGACAGTCCCTAGA	60	
DB	602 TTGTACCGAAGATGAGACCATCCAGGTGAAGGAAACGGCTAGTCGACAGTCCCTAGA	661	
QY	61 TTCCCGAACAGTACCCAGGAACTGCTCTGACATGGCGCTTCACTCTCAGGAGAA	120	
DB	662 TTCCCGAACAGTACCCAGGAACTGCTCTGACATGGCGCTTCACTCTCAGGAGAA	721	
QY	121 ACACGGATACAGTGTGTTGACATCAGTTGGATTAGGAGGACGAAATGATATC	180	
DB	722 ACACGGATACAGTGTGTTGACATCAGTTGGATTAGGAGGACGAAATGATATC	781	
QY	181 TGTAGTATGATTTGTGGAAGTTGAAGATATATCCGAAACAGTACCATTATTAGAGGA	240	
DB	782 TGTAGTATGATTTGTGGAAGTTGAAGATATATCCGAAACAGTACCATTATTAGAGGA	841	
QY	241 CGATGGTGGACACAAGGAAGTTCTCCAGGATAAAATCAAGAACGAACCAAAATTTAA	300	
DB	842 CGATGGTGGACACAAGGAAGTTCTCCAGGATAAAATCAAGAACGAACCAAAATTTAA	901	
QY	301 ATCATTTCAGTCCGATGACTTCTTGGCTAAACCTGGATTCAAGATTATTATCT	360	
DB	902 ATCATTTCAGTCCGATGACTTCTTGGCTAAACCTGGATTCAAGATTATTATCT	961	
QY	361 TTGCTGGAAGATTCCAAACCCGACGCTTCAGAGACCAACTGGGAATCTGTCAACAGC	420	
DB	962 TTGCTGGAAGATTCCAAACCCGACGCTTCAGAGACCAACTGGGAATCTGTCAACAGC	1021	
QY	421 TCTATTTCCAGGGATTCCTTAATCTCTCAATCAGTAACGGATCCCACTCTGATTGCGGAT	480	
DB	1022 TCTATTTCCAGGGATTCCTTAATCTCTCAATCAGTAACGGATCCCACTCTGATTGCGGAT	1081	
QY	481 GCTCTGGACAAAATTTGCAGAAATTTGATACAGTGGGAAGATCTGCTCAAGTACTTCAAT	540	
DB	1082 GCTCTGGACAAAATTTGCAGAAATTTGATACAGTGGGAAGATCTGCTCAAGTACTTCAAT	1141	
QY	541 CCAGAGTCAATGCAAGAAATCTTGAGAAATGATATCTGGACACCCCTCGGTATCGAGGC	600	
DB	1142 CCAGAGTCAATGCAAGAAATCTTGAGAAATGATATCTGGACACCCCTCGGTATCGAGGC	1201	

QY	601 AGGTCAATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG	660	
DB	1202 AGGTCAATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG	1261	
QY	661 GGTACAGTTGACCTCCAGGAATTTACTCGTCAATATAAGAGAGAGCTGAAGTTGGCC	720	
DB	1262 GGTACAGTTGACCTCCAGGAATTTACTCGTCAATATAAGAGAGAGCTGAAGTTGGCC	1321	
QY	721 AATGTGGTCTTCTTCCAGCTTGGCTCTCTGTCAGCCCTGTGGAGGAAATTTGGCTGT	780	
DB	1322 AATGTGGTCTTCTTCCAGCTTGGCTCTCTGTCAGCCCTGTGGAGGAAATTTGGCTGT	1381	
QY	781 GGAATCTCAATCTGGAGTCTGACATGCAATTCAGGGAACCGTCAAAAGTATCAT	840	
DB	1382 GGAATCTCAATCTGGAGTCTGACATGCAATTCAGGGAACCGTCAAAAGTATCAT	1441	
QY	841 GAGTATTACAGTTGAGCTGGCCACATCAAGAGGAGGGGTAGAGCTTAAGACCATGGCT	900	
DB	1442 GAGTATTACAGTTGAGCTGGCCACATCAAGAGGAGGGGTAGAGCTTAAGACCATGGCT	1501	
QY	901 CTAGTTCATCCAGTTGGATCAACATGACGATCCGATTTGATCTGAGCTCAAGACCA	960	
DB	1502 CTAGTTCATCCAGTTGGATCAACATGACGATTTGATCTGAGCTCAAGACCA	1561	
QY	961 CCTCGATAAGAGAATGTGCACATCTTACATTAAGCCCTGAAAGAACCTTTTAAAGGA	1020	
DB	1562 CCTCGATAAGAGAATGTGCACATCTTACATTAAGCCCTGAAAGAACCTTTTAAAGGA	1621	
QY	1021 GGGTGAGATAAGAGACCTTTTCTACAGCAACAACTTACTACTAGCTGCAATGCA	1080	
DB	1622 GGGTGAGATAAGAGACCTTTTCTACAGCAACAACTTACTACTAGCTGCAATGCA	1681	
QY	1081 ATGAACACAAGTGTGCTGAGTCTCAGCCCTTGTGTTAATGCCATGCCAAGTAGAAA	1140	
DB	1682 ATGAACACAAGTGTGCTGAGTCTCAGCCCTTGTGTTAATGCCAAGTAGAAA	1741	
QY	1141 GGTATATCATCAACTTCTATACCTAAGAAATATAGGATTTGCAATTAATAATAGTGTTCAG	1200	
DB	1742 GGTATATCATCAACTTCTATACCTAAGAAATATAGGATTTGCAATTAATAATAGTGTTCAG	1801	
QY	1201 GTTATATATGACAAACACACACACAGAAATATATTCATGTCTATGTATATATAGATCAAT	1260	
DB	1802 GTTATATATGACAAACACACACAGAAATATATTCATGTCTATGTATATATAGATCAAT	1861	
QY	1261 GTTTTTTTTGGTATATATAACAGGTACACAGAGCTTACATATGTTTGGTGTAGACTCT	1320	
DB	1862 GTTTTTTTTGGTATATATAACAGGTACACAGAGCTTACATATGTTTGGTGTAGACTCT	1921	
QY	1321 TAAATCTTTTCCAAATTAAGGGATGGTCAATATATATGAAACATGTCTTTAGAAAATTT	1380	
DB	1922 TAAATCTTTTCCAAATTAAGGGATGGTCAATATATATGAAACATGTCTTTAGAAAATTT	1981	
QY	1381 AGGAGATAAATTTTAAATTTTGAACACAAACAAATTTTGAATCTTCTCTCTTA	1440	
DB	1982 AGGAGATAAATTTTAAATTTTGAACACAAACAAATTTTGAATCTTCTCTCTTA	2041	
QY	1441 AAGAAAGCATCTCTGTATATTAATAATCAAAAGATGAGCTTCTTACATATACATCTTAG	1500	
DB	2042 AAGAAAGCATCTCTGTATATTAATAATCAAAAGATGAGCTTCTTACATATACATCTTAG	2101	
QY	1501 TTGATTTTAAAAAGGAAAAA --- GGTTCACAGAGAAAAAGGCCAATACCTTAAGCATTTT	1557	
DB	2102 TTGATTTTAAAAAGGAAAAAATGTTTCCAGAGAAAAAGGCCAATACCTTAAGCATTTT	2161	
QY	1558 TTCCATGAGAGCACTGCATCTTACCTATGTGACCTGTATACCTGTCTCCAAAACCA	1617	
DB	2162 TTCCATGAGAGCACTGCATCTTACCTATGTGACCTGTATACCTGTCTCCAAAACCA	2221	
QY	1618 TGCCATTAATATAAGTGTCTTTAGAAATTAATCATTTGTTGTTTTTATGCAATTTGCTG	1677	
DB	2222 TGCCATTAATATAAGTGTCTTTAGAAATTAATCATTTGTTGTTTTTATGCAATTTGCTG	2281	

QY 1678 AGGCATCCTTATTCATTTAAACACCTATCTCAAAACCTTACTTAGAAGGTTTTTATTATA 1737
Db |||||||
QY 2282 AGGCATGCTTATTCATTTAAACACCTATCTCAAAACCTTACTTAGAAGGTTTTTATTATA 2341
Db |||||||
QY 1738 GTCTCAAAAAGACAAATGTATAAGCTGTAAACAGAAATTTTGAATTTGTTTCTTTTGCAAAA 1797
Db GTCTCAAAAAGACAAATGTATAAGCTGTAAACAGAAATTTTGAATTTGTTTCTTTTGCAAAA 2401
QY 1798 CCCCTCACAAAAGCAAAATCTTTTCAAGAAATGGCATGGCAATCTGTATGAACCTTTTCCA 1857
Db CCCCTCACAAAAGCAAAATCTTTTCAAGAAATGGCATGGCAATCTGTATNNNNNNNNN 2461
QY 1858 GATGGTCTTCAGTCAAGAGTGTGGTAGTTGAGAACTTAAAGAGTGAACATTGAAACATC 1917
Db NNNNNNTTCAGTCAAGAGTGTGGTAGTTGAGAACTTAAAGAGTGAACATTGAAACATC 2521
QY 1918 GACGTAACCTGAAA 1931
Db GACGTAACCTGAAA 2535

RESULT 15

ID ADQ24013
XX ADQ24013 standard; DNA; 4153 BP.
AC ADQ24013;
XX
DT 26-AUG-2004 (first entry)
XX Human soft tissue sarcoma-upregulated DNA - SEQ ID 6833.

DE soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
KW ds.

XX Homo sapiens.

XX WO2004048938-A2.

XX 10-JUN-2004.

XX 26-NOV-2003; 2003WO-US038193.

XX 26-NOV-2002; 2002US-0429739P.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Aziz N, Ginsburg WM, Zlotnik A;

XX WPI; 2004-441208/41.

XX Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.

XX Example 2; SEQ ID NO 6833; 210pp; English.

XX The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC DNA of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.

XX Sequence 4153 BP; 1253 A; 855 C; 854 G; 1174 T; 0 U; 17 Other;

QY 1021 GGGTGAGATAAGAGACCCCTTTTCTCACGCAACCAAACTTACTACTAGCTGCAGTCA 1080

Query Match 98.08; Score 1896.2; DB 12; Length 4153;

Best Local Similarity 98.88; Pred. No. 0;

Matches 1911; Conservative 0; Mismatches 20; Indels 3; Gaps 1;

QY 1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAGAAACGGCTACGTGCAGAGTCTTAGA 60

Db TTGTACCGAAGAGATGAGACCATCCAGGTGAAGAAACGGCTACGTGCAGAGTCTTAGA 661

QY 61 TTCCGGAACAGCTACCCGAGAACCTGCTCTCTGACATGGCGGCTTCACTCTCAGAGAAAT 120

Db TTCCGGAACAGCTACCCGAGAACCTGCTCTCTGACATGGCGGCTTCACTCTCAGAGAAAT 721

QY 121 ACAGGGATCAGCTAGTGTGTAATCAGTTTGGATTAGAGGAGCAGAAATGATATC 180

Db ACAGGGATCAGCTAGTGTGTAATCAGTTTGGATTAGAGGAGCAGAAATGATATC 781

QY 181 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACAGTACCATTATTAGAGGA 240

Db TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACAGTACCATTATTAGAGGA 841

QY 241 CGATGGTGTGGACACAAAGGAAGTTCTTCCAAAGGATAAAATCAAGAACGAAACCAAAATTA 300

Db CGATGGTGTGGACACAAAGGAAGTTCTTCCAAAGGATAAAATCAAGAACGAAACCAAAATTA 901

QY 301 ATCATTCAAGTCCGATGACTACTTTTGGCTAAACCTGGATTCAAGATTATTATCT 360

Db ATCATTCAAGTCCGATGACTACTTTTGGCTAAACCTGGATTCAAGATTATTATCT 961

QY 361 TTGCTGGAAGATTTCCAAACCGCAGCAGCTTTCAGAGACCAACTGGGAATCTGTCAACAGC 420

Db TTGCTGGAAGATTTCCAAACCGCAGCAGCTTTCAGAGACCAACTGGGAATCTGTCAACAGC 1021

QY 421 TCTATTTTCAAGGGTATCCTATACTTCCATCAGTAACCGGATCCCACTCTGATTCGGAT 480

Db TCTATTTTCAAGGGTATCCTATACTTCCATCAGTAACCGGATCCCACTCTGATTCGGAT 1081

QY 481 GCTCTGACAAAAAATTTGAGAAATTTGATACAGTGGAGATCTGCTCAAGTACTTCAAT 540

Db GCTCTGACAAAAAATTTGAGAAATTTGATACAGTGGAGATCTGCTCAAGTACTTCAAT 1141

QY 541 CCAGAGTCATGGCAAGAAAGATCTTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC 600

Db CCAGAGTCATGGCAAGAAAGATCTTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC 1201

QY 601 AGGTCAATACATGACCGGAAGTCAAAAGTTGACCTCGATAGGCTCAATGATGATGCCAAG 660

Db AGGTCAATACATGACCGGAAGTCAAAAGTTGACCTCGATAGGCTCAATGATGATGCCAAG 1261

QY 661 CGTTACAGTTGCACTCCGAGGAATTTACTCGGTCAATATAGAGAGAGCTGAAGTTGGCC 720

Db CGTTACAGTTGCACTCCGAGGAATTTACTCGGTCAATATAGAGAGAGCTGAAGTTGGCC 1321

QY 721 AATGTGGTCTTTTCCACAGTTGCTCTCTCGTCAGCGCTGTGGAGGAAATTTGTGGCTGT 780

Db AATGTGGTCTTTTCCACAGTTGCTCTCTCGTCAGCGCTGTGGAGGAAATTTGTGGCTGT 1381

QY 781 GGAATCTCAATCTGAGGCTCTGCACATGCAATTCAGGAAACCGTGAAAAAGTATCAT 840

Db GGAATCTCAATCTGAGGCTCTGCACATGCAATTCAGGAAACCGTGAAAAAGTATCAT 1441

QY 841 GAGTATTAACAGTTTGAAGCTGGCCACATCAAGAGAGGGGTAGAGCTAAGACCATGGCT 900

Db GAGTATTAACAGTTTGAAGCTGGCCACATCAAGAGAGGGGTAGAGCTAAGACCATGGCT 1501

QY 901 CTAGTTCACATCCAGTTGGATCCATGAACGATTCGATTTCTATCGCAGCTCAAGACCA 960

Db CTAGTTCACATCCAGTTGGATCCATGAACGATTCGATTTCTATCGCAGCTCAAGACCA 1561

QY 961 CCTCGATAAGAGAAATGTGCACATCTTACATTAAAGCCCTGAAAGAACCTTTAGTTAAGGA 1020

Db CCTCGATAAGAGAAATGTGCACATCTTACATTAAAGCCCTGAAAGAACCTTTAGTTAAGGA 1621

```
Db      1622  GGGTGAATAAGAGACCCCTTTCCACAGCAACCAAACTTACTACTAGCCTGCAATGCA 1681
QY      1081  ATGAACACAAGTGGTTCAGTCTCAGGCTTCCTTTGTTAATGCGCATGGCAAGTAGAAA 1140
Db      1682  ATGAACACAAGTGGTTCAGTCTCAGGCTTCCTTTGTTAATGCGCATGGCAAGTAGAAA 1741
QY      1141  GGTATATCATCAACTTCTATACCTAGAAATATAGGATTCGATTTAATATAGTGTGAG 1200
Db      1742  GGTATATCATCAACTTCTATACCTAGAAATATAGGATTCGATTTAATATAGTGTGAG 1801
QY      1201  GTTATATATGCAAAAACACACACAGAAATATATTCATGTCATGTGTTATAGATCAAA 1260
Db      1802  GTTATATATGCAAAAACACACACAGAAATATATTCATGTCATGTGTTATAGATCAAA 1861
QY      1261  GTTTTTTTTGGTATATATACCAAGGTACACAGAGCTTACATATGTTTGAGTTAGACT 1320
Db      1862  GTTTTTTTTGGTATATATACCAAGGTACACAGAGCTTACATATGTTTGAGTTAGACT 1921
QY      1321  TAAATCCTTTGCAAAAATAAGGATGGTCAAAATATATGAAACATGCTCTTTAGAAAA 1380
Db      1922  TAAATCCTTTGCCAAAATAAGGATGGTCAAAATATATGAAACATGCTCTTTAGAAAA 1981
QY      1381  AGGAGATAAATTTATTTTAAATTTTGAACACAAAACAATTTGAACTCTGCTCTCTTA 1440
Db      1982  AGGAGATAAATTTATTTTAAATTTTGAACACAAAACAATTTGAACTCTGCTCTCTTA 2041
QY      1441  AAGAAAGCATCTGTATATTAATAATCAAAAGATGAGGCTTCTTACATATACATCTTAG 1500
Db      2042  AAGAAAGCATCTGTATATTAATAATCAAAAGATGAGGCTTCTTACATATACATCTTAG 2101
QY      1501  TTGATTATTAAAAAGGAAAAA- - -GGTTTCAGAGAAAAGGCCAATACCTAAGCATTTT 1557
Db      2102  TTGATTATTAAAAAGGAAAAATATGGTTTCAGAGAAAAGGCCAATACCTAAGCATTTT 2161
QY      1558  TTCCATGAGAAGCACTGCATCTTACCTATGTGGAATGTAATACCTGTCTCCAAAAACA 1617
Db      2162  TTCCATGAGAAGCACTGCATCTTACCTATGTGGAATGTAATACCTGTCTCCAAAAACA 2221
QY      1618  TCCCATATAATATAAGTCTTTAGAAATTAATCATTTGTTGTTTATGCAATTTTGCTG 1677
Db      2222  TCCCATATAATATAAGTCTTTAGAAATTAATCATTTGTTGTTTATGCAATTTTGCTG 2281
QY      1678  AGGCATCCTTATTCAATTTAAACACCTATCTCAAAAACTTACTTAGAAGGTTTTTATTATA 1737
Db      2282  AGGCATGCTTATTCAATTTAAACACCTATCTCAAAAACTTACTTAGAAGGTTTTTATTATA 2341
QY      1738  GTCCACAAAAAGCAATGTATAGCTGTAAACAGAAATTTGAAATGTTTCTTTGCAAAA 1797
Db      2342  GTCCACAAAAAGCAATGTATAGCTGTAAACAGAAATTTGAAATGTTTCTTTGCAAAA 2401
QY      1798  CCCCTCCCAAAAGCAAAATCCCTTTCAAGAAATGGCATGGCATCTCTGTATGAACCTTTCCA 1857
Db      2402  CCCCTCCCAAAAGCAAAATCCCTTTCAAGAAATGGCATGGCATCTCTGTATNNNNNNNNN 2461
QY      1858  GATGTGTTTCACTGAAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAACATTTGAAACATC 1917
Db      2462  NNNNNNGTTCACTGAAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAACATTTGAAACATC 2521
QY      1918  GACGTAACCTGGAAA 1931
Db      2522  GACGTAACCTGGAAA 2535
```

Search completed: October 31, 2004, 05:21:50
Job time : 895 secs

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OM protein - protein search, using sw model

Run on: October 29, 2004, 23:15:13 ; Search time 158 Seconds
(without alignments)
731.081 Million cell updates/sec

Title: US-10-086-623-6

Perfect score: 1742

Sequence: 1 LYRDETIQKNGYVQSPR.....DIQLDHHRCDCICSSRPPR 322

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1742	100.0	322	3 AAY71129	Aay71129 Human Pla
2	1742	100.0	347	7 ADK68120	Adk68120 Novel NOV
3	1742	100.0	364	4 AAU12264	Aau12264 Human PRO
4	1742	100.0	364	5 AAU15820	Aau15820 Human LP8
5	1742	100.0	364	5 ABB84973	Abb84973 Human PRO
6	1742	100.0	364	5 ABB95579	Abb95579 Human ang
7	1742	100.0	364	6 ABO17708	Abol7708 Novel hum
8	1742	100.0	364	6 ABU80962	Abu80962 Human PRO
9	1742	100.0	364	6 ABU66662	Abu66662 Human PRO
10	1742	100.0	364	6 ABU59743	Abu59743 Novel sec
11	1742	100.0	364	6 ABO24933	Abol24933 Human sec
12	1742	100.0	364	6 ABU66338	Abu66338 Human sec
13	1742	100.0	364	6 ADA45705	Ada45705 Novel hum
14	1742	100.0	364	6 ADA76136	Ada76136 Human PRO
15	1742	100.0	364	6 ADA18786	Ada18786 Human PRO
16	1742	100.0	364	6 ADA61409	Ada61409 Homo sapi
17	1742	100.0	364	6 ADB19194	Adb19194 Novel hum
18	1742	100.0	364	6 ADB27735	Adb27735 Human PRO
19	1742	100.0	364	6 ADA86214	Ada86214 Novel hum
20	1742	100.0	364	6 ADB15778	Adb15778 Human PRO
21	1742	100.0	364	6 ADA47564	Ada47564 Human PRO
22	1742	100.0	364	6 ADA67359	Ada67359 Human PRO
23	1742	100.0	364	6 ADB30366	Adb30366 Human PRO
24	1742	100.0	364	6 ADA85662	Ada85662 Novel hum
25	1742	100.0	364	6 ADA96874	Ada96874 Human PRO

26	1742	100.0	364	6 ADA79178	Ada79178 Human PRO
27	1742	100.0	364	6 ADA87317	Ada87317 Novel hum
28	1742	100.0	364	6 ADB16519	Adb16519 Human PRO
29	1742	100.0	364	6 ADA91611	Ada91611 Novel hum
30	1742	100.0	364	6 ADB14674	Adb14674 Human PRO
31	1742	100.0	364	6 ADB18635	Adb18635 Novel hum
32	1742	100.0	364	6 ADA93850	Ada93850 Human PRO
33	1742	100.0	364	6 ADB19746	Adb19746 Novel hum
34	1742	100.0	364	6 ADB13058	Adb13058 Human PRO
35	1742	100.0	364	6 ABO43241	Abo43241 Novel hum
36	1742	100.0	364	6 ADA74312	Ada74312 Human PRO
37	1742	100.0	364	6 ADB24545	Adb24545 Human PRO
38	1742	100.0	364	6 ADA82069	Ada82069 Human PRO
39	1742	100.0	364	6 ADA75032	Ada75032 Human PRO
40	1742	100.0	364	6 ADA85110	Ada85110 Novel hum
41	1742	100.0	364	6 ADA84558	Ada84558 Novel hum
42	1742	100.0	364	6 ADB29814	Adb29814 Human PRO
43	1742	100.0	364	6 ADA80342	Ada80342 Human PRO
44	1742	100.0	364	6 ADA75584	Ada75584 Human PRO
45	1742	100.0	364	6 ADA46809	Ada46809 Human PRO

ALIGNMENTS

RESULT 1

AAY71129

ID AAY71129 standard; peptide: 322 AA.

XX

AC AAY71129;

XX

DT 08-SEP-2000 (first entry)

XX

DE Human Platelet Derived Growth Factor (PDGF)-D partial polypeptide #2.

XX

KW Platelet Derived Growth Factor-D; PDGF-D; human; cytostatic; vulnary;

KW VEGF-G; Vascular Endothelial Growth Factor; antiatherosclerotic; tumour;

KW proliferative; activator; proliferation; differentiation; motility;

KW growth; PDGF-D receptor; antagonist; tissue remodelling; treat;

KW atherosclerosis; wound; metastasis.

XX

OS Homo sapiens.

XX

FN WO200027879-A1.

XX

PD 18-MAY-2000.

XX

PF 10-NOV-1999; 99WO-US026462.

XX

PR 10-NOV-1998; 98US-0107852P.

PR

28-DEC-1998; 98US-0113997P.

PR

26-AUG-1999; 99US-0150604P.

PR

04-OCT-1999; 99US-0157108P.

PR

05-OCT-1999; 99US-0157756P.

XX

(LUDW-) LUDWIG INST CANCER RES.

PA

(UYHE-) UNIV HELSINKI LICENSING LTD OY.

XX

Eriksson U, Aase K, Ponten A, Lee X, Uutela M, Alitalo K;

PI Oestman A, Heldin C;

XX

WPI; 2000-376495/32.

DR N-PSDB; AAD00737.

 XX |

Novel polynucleotides encoding a novel growth factor of cells expressing

PT a platelet-derived growth factor, useful for diagnostic and therapeutic

PT applications, e.g. concerning cancer.

XX

PS Claim 25; Fig 6; 11pp; English.

XX

The present sequence is an N-terminally truncated polypeptide of human

CC platelet derived growth factor (PDGF)-D, formally known as Vascular

CC Endothelial Growth Factor (VEGF)-G. It is derived from human foetal lung

CC lambdag10 cDNA library. It belongs to the VEGF/PDGF family. It functions
CC as an activator of proliferation, differentiation, growth and motility of
CC cells, that express PDGF-D receptor. This sequence is useful for
CC inhibiting the growth of tumours, that express PDGF-D. Expression of PDGF
CC-D and its proteolytic cleavage for generating an activated truncated
CC form is useful for regulating receptor binding specificity of PDGF-D.
CC PDGF-D antagonist is useful for inhibiting tissue remodelling during the
CC invasion of tumour cells into normal cells. PDGF-D may be used to treat
CC wounds, atherosclerosis, metastasis and migration of smooth muscle cells
XX
SQ Sequence 322 AA;

Query Match 100.0%; Score 1742; DB 3; Length 322;
Best Local Similarity 100.0%; Pred. No. 4.1e-166;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LYRDETIQVKGNGYVQSPFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLAEANDI 60
DB 1 LYRDETIQVKGNGYVQSPFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLAEANDI 60
QY 61 CRYDFVEVEDISSTIIIRGWCCHKEVPPIKSRNQIKITFKSDDYFVAKPGFKIYYS 120
DB 61 CRYDFVEVEDISSTIIIRGWCCHKEVPPIKSRNQIKITFKSDDYFVAKPGFKIYYS 120
QY 121 LLEDFOAAAASETWNESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVDELLKYFN 180
DB 121 LLEDFOAAAASETWNESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVDELLKYFN 180
QY 181 PESQWEDLENMVLDPYRGRSHDRKSKVDLDRLNDDAKRYSCPTPNYSVNIRELKIA 240
DB 181 PESQWEDLENMVLDPYRGRSHDRKSKVDLDRLNDDAKRYSCPTPNYSVNIRELKIA 240
QY 241 NVVFFPRCLLVORCGNGCCGTVNWRSCCTCNSGKTVKVKYHEVLQEPGHIKRRGAKTMA 300
DB 241 NVVFFPRCLLVORCGNGCCGTVNWRSCCTCNSGKTVKVKYHEVLQEPGHIKRRGAKTMA 300
QY 301 LVDIQLDHHRCDCICSSRPPR 322
DB 301 LVDIQLDHHRCDCICSSRPPR 322

RESULT 2

ID ADK68120 standard; protein; 347 AA.

AC ADK68120;

DT 06-MAY-2004 (first entry)

XX Novel NOVX protein #23.

XX antidiabetic; anorectic; cardiant; hypotensive; antiarteriosclerotic;
KW anorectic; virucide; antibacterial; fungicide; protozoacide; nootropic;
KW neuroprotective; antiparkinsonian; anticonvulsant; osteopathic;
KW antiarthritic; antiinflammatory; dermatological; antiasthmatic;
KW antilipemic; gene therapy; metabolic disorder; diabetes; obesity;
KW infectious disease; anorexia; cancer; cardiovascular disease;
KW hypertension; atherosclerosis; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder;
KW osteoarthritis; hematopoietic disorders; inflammatory skin disorder;
KW asthma; dyslipidemia; neurogenesis; cell differentiation;
KW cell proliferation; hematopoiesis; wound healing; angiogenesis;
KW chromosome mapping; pharmacogenomic.

XX Homo sapiens.

XX WO2003085124-A2.

XX 16-OCT-2003.

XX 01-APR-2003; 2003WO-US009775.

XX 01-APR-2002; 2002US-0369065P.

PR 05-APR-2002; 2002US-0370279P.
PR 05-APR-2002; 2002US-0370359P.
PR 08-APR-2002; 2002US-0370969P.
PR 12-APR-2002; 2002US-0372019P.
PR 22-APR-2002; 2002US-0374379P.
PR 15-MAY-2002; 2002US-0380973P.
PR 30-MAY-2002; 2002US-0384297P.
PR 30-MAY-2002; 2002US-0384329P.
PR 17-JUN-2002; 2002US-0389729P.
PR 13-AUG-2002; 2002US-0403491P.
PR 15-AUG-2002; 2002US-0403748P.
PR 31-MAR-2003; 2003US-00403142.
XX (CURA-) CURAGEN CORP.
XX
PI Alsobrook JP, Bento P, Boldog FL, Burgess CE, Caeman SJ;
PI Crabtree-Bokor JR, Edinger SR, Ellerman K, Fernandes BR, Gerlach VL;
PI Grosse WM, Gunther E, Gusev VY, Heyes MP, Lepley DM, Li L;
PI Macdougall JR, Malvankar UM, Millet I, Patturajan M, Peyman JA;
PI Rastelli L, Rieger DK, Shenoy SG, Shinkets RD, Smithson G, Stone DJ;
PI Vernet CAM, Voss EZ;
DR WPI; 2003-812730/76.
DR N-PSDB; ADK68119.
XX
PT New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
PT asthma, or infections.
PS Claim 1; SEQ ID NO 46; 323pp; English.

XX The invention relates to novel NOVX protein and their encoding DNA's,
CC mature forms of the proteins or sequences that are at least 95% identical
CC to, or having one or more conservative amino acid substitutions in, the
CC proteins. The polypeptides, nucleic acid molecules and antibodies are
CC useful in the manufacture of a medicament for treating a syndrome
CC associated with a human disease, preferably a NOVX-associated disorder.
CC The nucleic acid molecules, polypeptides and antibodies are useful for
CC treating, preventing or diagnosing diseases such as metabolic disorders,
CC diabetes, obesity, infectious diseases (viral, bacterial, fungal,
CC helminthic, and protozoal), anorexia, cancer, cardiovascular diseases
CC (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's
CC (osteoarthritis), hematopoietic disorders, inflammatory skin disorders,
CC asthma, and various dyslipidemias. The nucleic acids and polypeptides may
CC also be used as targets for the identification of small molecules that
CC modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
CC therapy, in generation of antibodies that bind immunospecifically to NOVX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridization probes, in chromosome mapping,
CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
CC corresponds to one of the NOVX proteins of the invention.

Sequence 347 AA;

Query Match 100.0%; Score 1742; DB 7; Length 347;
Best Local Similarity 100.0%; Pred. No. 4.7e-166;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LYRDETIQVKGNGYVQSPFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLAEANDI 60
DB 26 LYRDETIQVKGNGYVQSPFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLAEANDI 85
QY 61 CRYDFVEVEDISSTIIIRGWCCHKEVPPIKSRNQIKITFKSDDYFVAKPGFKIYYS 120
DB 86 CRYDFVEVEDISSTIIIRGWCCHKEVPPIKSRNQIKITFKSDDYFVAKPGFKIYYS 145
QY 121 LLEDFOAAAASETWNESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVDELLKYFN 180
DB 146 LLEDFOAAAASETWNESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVDELLKYFN 205

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QY 181 PESWQEDLENMYLDTPRYGRSGHYDRKSKVDLDRLLNDADAKRYSCPTPRNYSVNIREEKLA 240
DB 206 PESWQEDLENMYLDTPRYGRSGHYDRKSKVDLDRLLNDADAKRYSCPTPRNYSVNIREEKLA 265
QY 241 NVVFPFRCLLVQRCGCGCGTGVNWRSCVTKVKKYHEVLOPEPGHKKRGRAKTMA 300
DB 266 NVVFPFRCLLVQRCGCGCGTGVNWRSCVTKVKKYHEVLOPEPGHKKRGRAKTMA 325
QY 301 LVDIQLDHHERCDCICSSRPPR 322
DB 326 LVDIQLDHHERCDCICSSRPPR 347

RESULT 3
AAU12264
ID AAU12264 standard; protein; 364 AA.
XX
AC AAU12264;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human PRO4345 polypeptide sequence.
XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW A-peptide; factor VIIa; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200140466-A2.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US032678.
XX
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 30-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 11-FEB-2000; 2000WO-US000376.
PR 18-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
```

```
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Berezini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-408281/43.
DR N-PSDB; AAS21336.
XX
PT Isolated, secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT breast, prostate, cervical.
XX
PS Claim 12; Fig 186; 813pp; English.
XX
CC AAU12172-AAU12446 represent novel human secretory and transmembrane. PRO
CC polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO
CC polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumors by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 275 sequences are also useful to stimulate the release of tumour
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC differentiation of chondrocytes, the proliferation or gene expression in
CC pericyte cells, the release of proteoglycans from cartilage, the
CC proliferation of inner ear utricular supporting cells or of T-
CC lymphocytes, the release of a cytokine from peripheral blood monocytes
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC VIIa. The PRO polypeptides can be used in assays to identify molecules
CC involved in binding interactions. The polynucleotides encoding PRO
CC polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy
XX
SQ Sequence 364 AA;
```

```
Query Match 100.0%; Score 1742; DB 4; Length 364;
Best Local Similarity 100.0%; Pred. No. 5e-166;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 LYRDETIQVKGNGVQSPFPNSYPNLLLTWRLHSQENTRIQLVFNQFGLBEAENDI 60
DB 43 LYRDETIQVKGNGVQSPFPNSYPNLLLTWRLHSQENTRIQLVFNQFGLBEAENDI 102
QY 61 CRYDFVEVEDISSETTIIRGRWCGRHKEVPPIKSRTNQIKITFKSDDYFVAKPGFKIYYS 120
DB 103 CRYDFVEVEDISSETTIIRGRWCGRHKEVPPIKSRTNQIKITFKSDDYFVAKPGFKIYYS 162
QY 121 LLEDQFQAAASSETNWSVTSSISGVSYNPSVPTDPTLIADALDKKIAEFDTVEDLLKYFN 180
DB 163 LLEDQFQAAASSETNWSVTSSISGVSYNPSVPTDPTLIADALDKKIAEFDTVEDLLKYFN 222
QY 181 PESWQEDLENMYLDTPRYGRSGHYDRKSKVDLDRLLNDADAKRYSCPTPRNYSVNIREEKLA 240
DB 223 PESWQEDLENMYLDTPRYGRSGHYDRKSKVDLDRLLNDADAKRYSCPTPRNYSVNIREEKLA 282
QY 241 NVVFPFRCLLVQRCGCGCGTGVNWRSCVTKVKKYHEVLOPEPGHKKRGRAKTMA 300
DB 283 NVVFPFRCLLVQRCGCGCGTGVNWRSCVTKVKKYHEVLOPEPGHKKRGRAKTMA 342
QY 301 LVDIQLDHHERCDCICSSRPPR 322
DB 343 LVDIQLDHHERCDCICSSRPPR 364
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RESULT 4
AAE15820
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AAE15820 standard; protein; 364 AA.
AAE15820;
26-MAR-2002 (first entry)
Human LP85 protein #2.
LP85; platelet-derived growth factor; PDGF; antiinflammatory; vulnery;
osteoprotective; tranquilliser; musculoskeletal disorder;
MSD; therapy; bone growth; cartilage differentiation; wound healing;
neuron growth; bone fracture; osteoporosis; osteopenia; arthritis;
sarcopenia; periodontal disease; tissue atrophy; endocrine disorder;
muscle loss; immobility; bone density.
Homo sapiens.
Key Location/Qualifiers
FT Peptide 1..12
FT /label= Signal_peptide
FT Protein 13..364
FT /label= Human_mature_LP85_protein
WO200189450-A2.
29-NOV-2001.
08-MAY-2001; 2001WO-US011755.
19-MAY-2000; 2000US-0205424P.
11-JAN-2001; 2001US-0261071P.
11-JAN-2001; 2001US-0261076P.
(ELIL) LILLY & CO ELI.
Beals JM, Gonzalez-Dewhitt PA, Hammond LJ, Lu J, Na S, Su EW;
Witcher DR, Wroblewski VJ;
WPI; 2002-083040/11.
N-PSDB; AAD25489.
Analog of a platelet-derived growth factor homolog, LP85 useful for
treating osteoporosis, arthritis, sarcopenia, wounds, has one or more
amino acid substitutions which destroy the tripeptidyl sequence of native
LP85.
Disclosure; Page 114-115; 117pp; English.
The present invention relates to LP85, an analogue of platelet-derived
growth factor (PDGF) homologue. Sequences of the invention are useful for
the manufacture of a medicament for treating musculoskeletal disorder
(MSD) which include promoting bone growth, cartilage differentiation and
function, wound healing, neuron growth, preventing cartilage degradation
or neuronal degeneration. They are useful for treating bone fractures,
osteoporosis, osteopenia, arthritis, sarcopenia, periodontal disease,
tissue atrophy, traumatised connective tissues, grafted connective
tissues and/or transplanted organs, bone or muscle loss due to
malignancy, endocrine disorders and immobility. They are also used for
prophylactically increasing or maintaining bone density in a mammal. The
present sequence is human LP85 protein
Sequence 364 AA;
Query Match 100.0%; Score 1742; DB 5; Length 364;
Best Local Similarity 100.0%; Pred. No. 5e-166;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 LYRRDETIQKNGYVQSPFRFNSPRNLLLTWRLHSQENTRIQLVFDNQFGLAEANDI 60
43 LYRRDETIQKNGYVQSPFRFNSPRNLLLTWRLHSQENTRIQLVFDNQFGLAEANDI 102
61 CRYDFVEVEDISSTIIRGWCCHKEVPPRIKGRTNQIKITFKSDDYFVAKPGPKIYYS 120
|||||

Db 103 CRYDFVEVEDISSTIIRGWCCHKEVPPRIKGRTNQIKITFKSDDYFVAKPGPKIYYS 162
QY 121 LLEDQPAAASSETNWESVTSSISGVSYNSPSVPTPTLIADALDKKIAEFDEVDLLKYFN 180
|||
Db 163 LLEDQPAAASSETNWESVTSSISGVSYNSPSVPTPTLIADALDKKIAEFDEVDLLKYFN 222
|||
QY 181 PESWQEDLENMYLDTPRYGRGSYHDKRSKVDLDRINDDAKRYSCTPRNSYNIREELKLA 240
|||
Db 223 PESWQEDLENMYLDTPRYGRGSYHDKRSKVDLDRINDDAKRYSCTPRNSYNIREELKLA 282
|||
QY 241 NVVFFPRCLLVORCGNGCGCTVNWRSCTCNSGKTVKKYHEVLOPEPGHKKRGRAKTMA 300
|||
Db 283 NVVFFPRCLLVORCGNGCGCTVNWRSCTCNSGKTVKKYHEVLOPEPGHKKRGRAKTMA 342
|||
QY 301 LVDIQLDHHERCDCICSSRPPR 322
|||
Db 343 LVDIQLDHHERCDCICSSRPPR 364
|||
RESULT 5
ABB84973
ID ABB84973 standard; protein; 364 AA.
XX
AC ABB84973;
XX
DT 16-MAY-2002 (first entry)
XX
DE Human PRO4345 protein sequence SEQ ID NO:314.
XX
KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
gene therapy; cardiovascular disorder; endothelial disorder; cancer;
angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
age-related macular degeneration; arterial restenosis; angina;
rheumatoid arthritis; myocardial infarction; thrombophlebitis;
lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
wound healing; chromosome mapping; gene mapping.
XX
OS Homo sapiens.
XX
PN WO200200690-A2.
XX
PD 03-JAN-2002.
XX
PF 20-JUN-2001; 2001WO-US019692.
XX
PR 23-JUN-2000; 2000US-0213637P.
PR 25-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 28-JUL-2000; 2000US-0220664P.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.

PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
XX Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX WPI: 2002-171999/22.
DR N-PSDB; ABL95717.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
XX Claim 11; Fig 314; 567pp; English.
PS
XX The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a PRO protein of the invention
XX
XX Sequence 364 AA;
SQ
Query Match 100.0%; Score 1742; DB 5; Length 364;
Best Local Similarity 100.0%; Pred. No. 5e-166;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LYRRDETIOKNGYVQSPFRFNSYPRNLLLTWRHLSQENTRIQLVFDNQFGLAEANDI 60
DB 43 LYRRDETIOKNGYVQSPFRFNSYPRNLLLTWRHLSQENTRIQLVFDNQFGLAEANDI 102
QY 61 CRYDFEVEDEDISTSTIIRGRWCGHKEVPPRIKSRNQIKITFKSDDFVAKPGFKIYYS 120
DB 103 CRYDFEVEDEDISTSTIIRGRWCGHKEVPPRIKSRNQIKITFKSDDFVAKPGFKIYYS 162
QY 121 LLEDQFAAAATNESVTSISGVSYNSPSTVDPTLIADALDKKIAEPTVEDLLKYPN 180
DB 163 LLEDQFAAAATNESVTSISGVSYNSPSTVDPTLIADALDKKIAEPTVEDLLKYPN 222
QY 181 PESQWEDLENNYLDTPRYGRSHYHDKSKVDLDRINDAKRYSCTPRNYSVNIREEKLA 240
DB 223 PESQWEDLENNYLDTPRYGRSHYHDKSKVDLDRINDAKRYSCTPRNYSVNIREEKLA 282
QY 241 NVVFPRLCLLVORCGNCCGCTVNNRSCTCNSGKTVKKYHEVLQEPGHIKRRGAKTWA 300
DB 283 NVVFPRLCLLVORCGNCCGCTVNNRSCTCNSGKTVKKYHEVLQEPGHIKRRGAKTWA 342
QY 301 LVDIQLDHERCDCICSSRPPR 322
DB 343 LVDIQLDHERCDCICSSRPPR 364
RESULT 7
ID ABO17708 standard; protein; 364 AA.
XX ABO17708;
AC ABO17708;
XX
XX 26-AUG-2003 (first entry)
DT
XX
XX Novel human secreted and transmembrane protein PRO4345.
DE
DE Human; secreted and transmembrane protein; PRO; anti-inflammatory;
KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
KW TNF-alpha release; cell proliferation; cell differentiation;
KW gene expression modulator; proteoglycan release; cytokine release;
KW tumour; inflammatory disease; organ failure; atherosclerosis;
KW cardiac injury; infertility; birth defect; premature aging; AIDS;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
KW bioreactor; tissue typing.

XX Homo sapiens.
OS US2003032156-A1.
XX
XX 13-FEB-2003.
PD
XX
XX 06-MAY-2002; 2002US-00140474.
PF
XX
XX 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 05-JAN-2000; 99WO-US031274.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.

23-AUG-2000; 2000WO-US023522.
24-AUG-2000; 2000WO-US023328.
28-NOV-2000; 2000WO-US030952.
10-NOV-2000; 2000WO-US030873.
01-DEC-2000; 2000WO-US032678.
20-DEC-2000; 2000US-00747259.
20-DEC-2000; 2000WO-US034956.
28-FEB-2001; 2001US-00796498.
28-FEB-2001; 2001WO-US006520.
01-MAR-2001; 2001WO-US006666.
09-MAR-2001; 2001US-00802706.
14-MAR-2001; 2001US-00808689.
22-MAR-2001; 2001US-00816744.
05-APR-2001; 2001US-00828366.
10-MAY-2001; 2001US-00854208.
10-MAY-2001; 2001US-00854280.
18-MAY-2001; 2001US-00860216.
25-MAY-2001; 2001US-00866028.
25-MAY-2001; 2001US-00866034.
25-MAY-2001; 2001WO-US017092.
01-JUN-2001; 2001US-00872035.
01-JUN-2001; 2001WO-US017800.
05-JUN-2001; 2001US-00874503.
14-JUN-2001; 2001US-00882636.
19-JUN-2001; 2001US-00886342.
20-JUN-2001; 2001WO-US019692.
21-JUN-2001; 2001US-00887879.
22-JUN-2001; 2001WO-US020116.
29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
18-JUL-2001; 2001US-00908827.
06-AUG-2001; 2001US-00924419.
09-AUG-2001; 2001US-00927796.
16-AUG-2001; 2001US-00931836.
19-DEC-2001; 2001US-00028072.
(GETH) GENENTECH INC.
Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
Geritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
WPI; 2003-341980/32.
N-PSDB; ACD23945.
New secreted and transmembrane PRO nucleic acids, for treating
inflammation, organ failure, atherosclerosis, cardiac injury,
infertility, birth defects, premature aging, acquired immunodeficiency
syndrome (AIDS), or cancer.
Claim 12; Fig 186; 660pp; English.
The invention describes an isolated nucleic acid (I) comprising, or which
has 80 % sequence identity to, or the full-length coding sequence of, one
of 275 nucleotide sequences, and which encodes a corresponding
polypeptide selected from 275 amino acid sequences, where all sequences
are given in the specification. The polypeptide encoded by (I) is used to
detect PRO polypeptides, link a bioactive molecule to a cell expressing a
PRO polypeptide, modulate a biological activity of a cell, stimulate the
release of tumour necrosis factor (TNF)-alpha from human blood, modulate
the uptake of glucose or free fatty acid by cells, stimulate or inhibit
the proliferation or differentiation of cells or gene expression,
stimulate the release of proteoglycans, stimulate the release of cytokine
from peripheral blood mononuclear cells, inhibit the binding of A-peptide
to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
acid and polypeptide encoded by (I), are useful for treating inflammatory
diseases, organ failure, atherosclerosis, cardiac injury, infertility,
birth defects, premature aging, acquired immunodeficiency syndrome
(AIDS), cancer, or diabetic complications. The nucleic acid is useful as
hybridisation probes, in chromosome and gene mapping, and in generating
antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
This is the amino acid sequence of a novel human secreted and

CC transmembrane PRO polypeptide
XX Sequence 364 AA;
SQ
Query Match 100.0%; Score 1742; DB 6; Length 364;
Best Local Similarity 100.0%; Pred. No. 5e-166;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LYRDETIQVKGNGYVQSPFPNSYPRLNLLTWLHSGQENTRIQLVFDNQFGLSEAEENDI 60
Db 43 LYRDETIQVKGNGYVQSPFPNSYPRLNLLTWLHSGQENTRIQLVFDNQFGLSEAEENDI 102
Qy 61 CRVDFVEVEDISSTIIIRGWCHEVPRIKSRNTQIKITFKSDDYFVAKPGFKIYYS 120
Db 103 CRVDFVEVEDISSTIIIRGWCHEVPRIKSRNTQIKITFKSDDYFVAKPGFKIYYS 162
Qy 121 LLEDQFAAASATNWSVTSSISGVSYNSPSVPTDPTLIADALDKKIAEFDVDELLKYFN 180
Db 163 LLEDQFAAASATNWSVTSSISGVSYNSPSVPTDPTLIADALDKKIAEFDVDELLKYFN 222
Qy 181 PESQEDLENNYLDTPRYGRSHYDRKSKVDLRLNDADAKRYSCPTPRNYSVNIIEELKLA 240
Db 223 PESQEDLENNYLDTPRYGRSHYDRKSKVDLRLNDADAKRYSCPTPRNYSVNIIEELKLA 282
Qy 241 NVVFFPRLVQRCGNGCGCTVNNRSTCNSGKTVKKYHEVLOFEPGHIKRRGRKATMA 300
Db 283 NVVFFPRLVQRCGNGCGCTVNNRSTCNSGKTVKKYHEVLOFEPGHIKRRGRKATMA 342
Qy 301 LVDIQLDHERCDCICSSRPPR 322
Db 343 LVDIQLDHERCDCICSSRPPR 364
RESULT 8
ABU80962
ID ABU80962 standard; protein; 364 AA.
XX AC ABU80962;
XX DT 23-JUN-2003 (first entry)
XX DE Human PRO polypeptide #93.
XX KW Human; PRO polypeptide; secreted and transmembrane protein;
KW anti-PRO antibody; diagnostic assay; gene expression; diabetes;
KW bone disorder; cartilage disorder; rheumatoid arthritis; obesity;
KW sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;
KW hearing loss; coagulation disorder; stroke; heart attack; cardiac;
KW antididiabetic; anorectic; vulnery; antiarthritic; osteopathic;
KW antirheumatic; auditory; cerebroprotective; angiogenic.
OS Homo sapiens.
XX US2003004311-A1.
XX PN 02-JAN-2003.
XX PD 19-DEC-2001; 2001US-00028072.
XX PF 18-JUN-1997; 97US-0049911P.
XX PR 26-AUG-1997; 97US-0056974P.
XX PR 17-SEP-1997; 97US-0059113P.
XX PR 17-SEP-1997; 97US-0059115P.
XX PR 17-SEP-1997; 97US-0059117P.
XX PR 17-SEP-1997; 97US-0059122P.
XX PR 17-SEP-1997; 97US-0059184P.
XX PR 18-SEP-1997; 97US-0059263P.
XX PR 19-SEP-1997; 97US-0059352P.
XX PR 24-SEP-1997; 97US-0059588P.
XX PR 17-OCT-1997; 97US-0059836P.
XX PR 17-OCT-1997; 97US-0062250P.
XX PR 17-OCT-1997; 97US-0062285P.
XX PR 17-OCT-1997; 97US-0062287P.


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PR 17-OCT-1997; 97US-0063755P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063082P.
PR 24-OCT-1997; 97US-0063127P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063561P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063733P.
PR 29-OCT-1997; 97US-0063735P.
PR 03-NOV-1997; 97US-0063738P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066701P.
PR 11-DEC-1997; 97US-0069212P.
PR 11-DEC-1997; 97US-0069278P.
PR 11-DEC-1997; 97US-0069334P.
PR 16-DEC-1997; 97US-0069694P.
PR 23-JAN-1998; 98US-0072320P.
PR 04-FEB-1998; 98US-0073122P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 12-MAR-1998; 98US-0077791P.
PR 20-MAR-1998; 98US-0078910P.
PR 25-MAR-1998; 98US-0079294P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079728P.
PR 31-MAR-1998; 98US-0080165P.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 16-SEP-1998; 98WO-US019177.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 98WO-US000106.
PR 08-MAR-1999; 98WO-US005028.
PR 10-MAR-1999; 98WO-US005190.
PR 20-APR-1999; 98WO-US008615.
PR 14-MAY-1999; 98WO-US010733.
PR 02-JUN-1999; 98WO-US012252.
PR 01-SEP-1999; 98WO-US020111.
PR 08-SEP-1999; 98WO-US020594.
PR 13-SEP-1999; 98WO-US020944.
PR 15-SEP-1999; 98WO-US021090.
PR 15-SEP-1999; 98WO-US021547.
PR 05-OCT-1999; 98WO-US023089.
PR 29-NOV-1999; 98WO-US028214.
PR 30-NOV-1999; 98WO-US028313.
PR 30-NOV-1999; 98WO-US028409.
PR 01-DEC-1999; 98WO-US028301.
PR 01-DEC-1999; 98WO-US028634.
PR 02-DEC-1999; 98WO-US028551.
PR 02-DEC-1999; 98WO-US028564.
PR 16-DEC-1999; 98WO-US028565.
PR 16-DEC-1999; 98WO-US030095.
PR 20-DEC-1999; 98WO-US030911.
PR 20-DEC-1999; 98WO-US030999.

PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.

PA (GETH ) GENENTECH INC.
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI: 2003-352836/33.
DR N-PSDB; ACA67086.
XX
PT New isolated PRO polypeptide useful for treating diabetes, rheumatoid
PT arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or
PT heart attack.
XX
PS Claim 12; Fig 186; 643pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the treatment of diabetes, bone and/or cartilage disorders
CC (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,
CC hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders
CC (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic
CC assays for PRO, by detecting its expression in specific cells, tissues or
CC serum, and for affinity purification of PRO from recombinant cell culture
CC or natural sources. AB080870-AB081144 represent the human PRO
CC polypeptides of the invention. Note: The sequence data for this patent
CC was obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/paipsDIDentry.html
XX
SQ Sequence 364 AA;
Query Match 100.0%; Score 1742; DB 6; Length 364;
Best Local Similarity 100.0%; Pred. No. 5e-166; Mismatches 0; Gaps 0;
Matches 322; Conservative 0; Indels 0;

QY 1 LYRDETTIQVKGNGYVQSPRPNSYPNLLLTWRHLSQENTRIQLVFDNQFGLAEANDI 60
DB |||||||
QY 43 LYRDETTIQVKGNGYVQSPRPNSYPNLLLTWRHLSQENTRIQLVFDNQFGLAEANDI 102
DB |||||||
QY 61 CRYDFVEVEDISETSTIIRGRWCCHKEVPPRIKSTNOIKITFKSDDYFVAKPGPKIYYS 120
DB |||||||
QY 103 CRYDFVEVEDISETSTIIRGRWCCHKEVPPRIKSTNOIKITFKSDDYFVAKPGPKIYYS 162
QY 121 LLEDQPAASATNWESVTSISGVSYNSPSVTDPTLTADALDKKIAEFTVDELLKYFN 180
DB |||||||
QY 163 LLEDQPAASATNWESVTSISGVSYNSPSVTDPTLTADALDKKIAEFTVDELLKYFN 222
QY 181 PESWQEDLENNYLDTPRYGRSYHDKRSKVDLRLNDLNDKAKRYSCTPRNSYNVIREELKIA 240
DB |||||||
QY 223 PESWQEDLENNYLDTPRYGRSYHDKRSKVDLRLNDLNDKAKRYSCTPRNSYNVIREELKIA 282
QY 241 NVVFPFRCCLLVQRCGNGCGGTWNWRSCTCNSGKTKYKHYEVLPQEPGHIKRRGAKTMA 300
DB |||||||
QY 283 NVVFPFRCCLLVQRCGNGCGGTWNWRSCTCNSGKTKYKHYEVLPQEPGHIKRRGAKTMA 342
QY 301 LVDIOLDHHERCDICSSRRPR 322
DB |||||||
QY 343 LVDIOLDHHERCDICSSRRPR 364
```

RESULT 9

ABU66662

ID ABU66662 standard; protein; 364 AA.

XX AC

XX AC

XX AC

DT 23-MAY-2003 (first entry)

XX DE

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XX DE

XX DE

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XX DE

Human; PRO polypeptide; secreted and transmembrane protein;
tumour necrosis factor-alpha; TNF-alpha; blood, proliferation;
differentiation; chondrocyte; tumour; genetic disorder; cytostatic.

OS Homo sapiens.

XX US2003036180-A1.

XX 20-FEB-2003.

XX 09-MAY-2002; 2002US-00143114.

XX 31-MAR-1997; 97WO-US005230.

XX 12-JUN-1998; 98WO-US012456.

XX 14-JUL-1998; 98WO-US014552.

XX 28-AUG-1998; 98WO-US017888.

XX 10-SEP-1998; 98WO-US018824.

XX 14-SEP-1998; 98WO-US019093.

XX 14-SEP-1998; 98WO-US019094.

XX 14-SEP-1998; 98WO-US019177.

XX 16-SEP-1998; 98WO-US019330.

XX 17-SEP-1998; 98WO-US019437.

XX 07-OCT-1998; 98WO-US021141.

XX 29-OCT-1998; 98WO-US022992.

XX 20-NOV-1998; 98WO-US024855.

XX 01-DEC-1998; 98WO-US025108.

XX 05-JAN-1999; 99WO-US000106.

XX 08-MAR-1999; 99WO-US005028.

XX 10-MAR-1999; 99WO-US005190.

XX 20-APR-1999; 99WO-US008615.

XX 14-MAY-1999; 99WO-US010733.

XX 02-JUN-1999; 99WO-US012252.

XX 01-SEP-1999; 99WO-US020111.

XX 08-SEP-1999; 99WO-US020594.

XX 13-SEP-1999; 99WO-US020944.

XX 15-SEP-1999; 99WO-US021090.

XX 15-SEP-1999; 99WO-US021547.

XX 05-OCT-1999; 99WO-US023089.

XX 29-NOV-1999; 99WO-US028214.

XX 30-NOV-1999; 99WO-US028313.

XX 30-NOV-1999; 99WO-US028409.

XX 01-DEC-1999; 99WO-US028301.

XX 01-DEC-1999; 99WO-US028634.

XX 02-DEC-1999; 99WO-US028551.

XX 02-DEC-1999; 99WO-US028564.

XX 02-DEC-1999; 99WO-US028565.

XX 16-DEC-1999; 99WO-US030095.

XX 20-DEC-1999; 99WO-US030911.

XX 20-DEC-1999; 99WO-US030999.

XX 22-DEC-1999; 99WO-US030720.

XX 30-DEC-1999; 99WO-US031243.

XX 30-DEC-1999; 99WO-US031274.

XX 05-JAN-2000; 2000WO-US000219.

XX 06-JAN-2000; 2000WO-US000277.

XX 06-JAN-2000; 2000WO-US000376.

XX 11-FEB-2000; 2000WO-US003565.

XX 18-FEB-2000; 2000WO-US004341.

XX 18-FEB-2000; 2000WO-US004342.

XX 22-FEB-2000; 2000WO-US004414.

XX 24-FEB-2000; 2000WO-US004914.

PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032878.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.

(GETH) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritken ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-332040/31.

N-PSDB; ACA03695.

XX New secreted and transmembrane PRO nucleic acids, useful for gene
PT therapy, in chromosome and gene mapping, as chromosome markers, in tissue
PT typing, and in chromosome identification.

XX Claim 12; Fig 186; 660pp; English.

XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for
CC identifying agonists or antagonists. The PRO polypeptides are useful for

CC for stimulating the release of tumour necrosis factor (TNF)-alpha from
CC human blood, for stimulating the proliferation or differentiation of
CC chondrocytes, and detecting the presence of tumours. The polynucleotide
CC sequences encoding PRO polypeptides are useful as hybridisation probes,
CC in chromosome and gene mapping, in the generation of antisense RNA and
CC DNA, in the preparation of PRO polypeptides, for generating transgenic
CC animals or knockout animals, for the genetic analysis of individuals with
CC genetic disorders, and in gene therapy. ABU66570-ABU6844 represent the
CC human PRO polypeptides of the invention. Note: The sequence data for this
CC patent was obtained in electronic format directly from the USPTO web site
CC at seqdata.uspto.gov/psipdb/entry.html
XX
SQ Sequence 364 AA;

Query Match 100.0%; Score 1742; DB 6; Length 364;
Best Local Similarity 100.0%; Pred. No. 5e-166;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LYRRDETQVKGNGYVQSPFPNSYPRNLLLTWRLHSENTRIQLVFNQFGLAEANDI 60
Db 43 LYRRDETQVKGNGYVQSPFPNSYPRNLLLTWRLHSENTRIQLVFNQFGLAEANDI 102
QY 61 CRYDFVEVEDISSETIIRGRWCGHKEVPPRIKSRNQIKITFKSDDYFVAKPGFKIYYS 120
Db 103 CRYDFVEVEDISSETIIRGRWCGHKEVPPRIKSRNQIKITFKSDDYFVAKPGFKIYYS 162
QY 121 LLEDQPAASSTNVESTSSISGVNSPSVTDPTLIADALDKKIASEFTVDELLKYFN 180
Db 163 LLEDQPAASSTNVESTSSISGVNSPSVTDPTLIADALDKKIASEFTVDELLKYFN 222
QY 181 PESWQEDLENMYYLDTPRYGRSVDHDKSKVDLDRLNDDAKRYSCTPRNSVNIIEELKLA 240
Db 223 PESWQEDLENMYYLDTPRYGRSVDHDKSKVDLDRLNDDAKRYSCTPRNSVNIIEELKLA 282
QY 241 NVVFPRLVORCGNGCGGVNWRSCNCGTKVKKYHEVLQEPGHIKRGRAKMA 300
Db 283 NVVFPRLVORCGNGCGGVNWRSCNCGTKVKKYHEVLQEPGHIKRGRAKMA 342
QY 301 LVDIQLDHHERCDCICSSRPPR 322
Db 343 LVDIQLDHHERCDCICSSRPPR 364

RESULT 10

ABU59743
ID ABU59743 standard; protein; 364 AA.

XX AC ABU59743;

XX DT 13-MAY-2003 (first entry)

XX DE Novel secreted and transmembrane protein PR04345.

XX KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.

XX OS Homo sapiens.

XX PN US2003017563-A1.

XX PD 23-JAN-2003.

XX PF 07-MAY-2002; 2002US-00140808.

XX PR 31-MAR-1997; 97WO-US005230.

PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 29-OCT-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 98WO-US000106.
PR 08-MAR-1999; 98WO-US005028.
PR 10-MAR-1999; 98WO-US005190.
PR 20-APR-1999; 98WO-US008615.
PR 14-MAY-1999; 98WO-US010733.
PR 02-JUN-1999; 98WO-US012252.
PR 01-SEP-1999; 98WO-US020111.
PR 08-SEP-1999; 98WO-US020594.
PR 13-SEP-1999; 98WO-US020944.
PR 15-SEP-1999; 98WO-US021090.
PR 15-SEP-1999; 98WO-US021547.
PR 05-OCT-1999; 98WO-US023089.
PR 29-NOV-1999; 98WO-US028214.
PR 30-NOV-1999; 98WO-US028313.
PR 30-NOV-1999; 98WO-US028409.
PR 01-DEC-1999; 98WO-US028301.
PR 01-DEC-1999; 98WO-US028634.
PR 02-DEC-1999; 98WO-US028551.
PR 02-DEC-1999; 98WO-US028564.
PR 02-DEC-1999; 98WO-US028565.
PR 16-DEC-1999; 98WO-US030095.
PR 20-DEC-1999; 98WO-US030911.
PR 20-DEC-1999; 98WO-US030999.
PR 22-DEC-1999; 98WO-US030720.
PR 30-DEC-1999; 98WO-US031243.
PR 30-DEC-1999; 98WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.

PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 18-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001US-00866034.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001US-00872035.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001US-00886342.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001US-00887879.
PR 29-JUN-2001; 2001US-00921066.
PR 09-JUL-2001; 2001US-00921735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
PA (GETH) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;
XX
DR WPI; 2003-148238/14.
DR N-PSDB; ABX89233.
XX
XX Two hundred and seventy five nucleic acids encoding PRO polypeptides,
PT useful for treating pericyte-associated tumors, diabetes and various bone
PT and/or cartilage disorders, e.g. arthritis.
XX
XX Claim 12; Fig 186; 659pp; English.
XX
XX The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumors. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
CC and PRO11066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This is the
CC amino acid sequence of a novel human PRO protein
XX Sequence 364 AA;
SQ

Query Match 100.0%; Score 1742; DB 6; Length 364;
Best Local Similarity 100.0%; Pred. No. 5e-166;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LYRDETIQVKGNGYVQSPFPNSYPRNLLLTWRLHSGENTRIQLVFNQFGLGEAEANDI 60
DB 43 LYRDETIQVKGNGYVQSPFPNSYPRNLLLTWRLHSGENTRIQLVFNQFGLGEAEANDI 102
QY 61 CRYDFVEVEDISSETTIIRGRWCCHKEVPPIKSRITNQIKITPKSDDDYFVAKPGFKIYYS 120
DB 103 CRYDFVEVEDISSETTIIRGRWCCHKEVPPIKSRITNQIKITPKSDDDYFVAKPGFKIYYS 162
QY 121 LLEDFOFAAASSETNWESVTSSISGVSYNSPSVTPPTLIADALDKKIAEFDTVEDLLKYFN 180
DB 163 LLEDFOFAAASSETNWESVTSSISGVSYNSPSVTPPTLIADALDKKIAEFDTVEDLLKYFN 222
QY 181 PESWQEDLENNYLDTPYRGRSYHDKRSKVLDRLNDDAKYSCTPRNYSVNIIEELKLA 240
DB 223 PESWQEDLENNYLDTPYRGRSYHDKRSKVLDRLNDDAKYSCTPRNYSVNIIEELKLA 282
QY 241 NVVFFPRCLLVQRCGNGCGCTVNMRSCTCNSGKTVKYYHEVLQFEPGHIKRRGSAKTM 300
DB 283 NVVFFPRCLLVQRCGNGCGCTVNMRSCTCNSGKTVKYYHEVLQFEPGHIKRRGSAKTM 342
QY 301 LVDIQLDHERCDCICSSRPPR 322
DB 343 LVDIQLDHERCDCICSSRPPR 364
RESULT 11
ABO24933
ID ABO24933 standard; protein; 364 AA.
XX AC ABO24933;
XX
XX DT 05-SEP-2003 (first entry)
XX DE Human secreted/transmembrane protein (PRO) #93.
XX KW Human; PRO; secreted protein; transmembrane protein; tumour; cytostatic;
KW gene therapy; tumour necrosis factor-alpha; TNF-alpha; blood;
KW proteoglycan; cartilage; cytokine; peripheral blood mononuclear cell;
KW FMC; glucose uptake; PFA; skeletal muscle cell; adipocyte cell;
KW chondrocyte cell proliferation; chondrocyte cell differentiation;
KW pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell;
XX endothelial cell; A-peptide; factor VIIA.
OS Homo sapiens.
XX
XX US2003036179-A1.
XX PD 20-FEB-2003.
XX PF 10-MAY-2002; 2002US-00142431.
XX PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 16-SEP-1998; 98WO-US019177.
PR 17-SEP-1998; 98WO-US019330.
PR 07-OCT-1998; 98WO-US019437.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.

20-APR-1999; 99WO-US0008615.
 14-MAY-1999; 99WO-US010733.
 02-JUN-1999; 99WO-US013252.
 01-SEP-1999; 99WO-US020111.
 08-SEP-1999; 99WO-US020594.
 13-SEP-1999; 99WO-US020944.
 15-SEP-1999; 99WO-US021090.
 15-SEP-1999; 99WO-US021547.
 05-OCT-1999; 99WO-US023089.
 28-NOV-1999; 99WO-US028214.
 30-NOV-1999; 99WO-US028313.
 30-NOV-1999; 99WO-US028409.
 01-DEC-1999; 99WO-US028301.
 01-DEC-1999; 99WO-US028634.
 02-DEC-1999; 99WO-US028551.
 02-DEC-1999; 99WO-US028564.
 02-DEC-1999; 99WO-US028565.
 16-DEC-1999; 99WO-US030095.
 20-DEC-1999; 99WO-US030911.
 20-DEC-1999; 99WO-US030999.
 22-DEC-1999; 99WO-US030720.
 30-DEC-1999; 99WO-US031243.
 30-DEC-1999; 99WO-US031274.
 05-JAN-2000; 2000WO-US000219.
 06-JAN-2000; 2000WO-US000277.
 11-FEB-2000; 2000WO-US000376.
 18-FEB-2000; 2000WO-US003565.
 18-FEB-2000; 2000WO-US004341.
 22-FEB-2000; 2000WO-US004342.
 24-FEB-2000; 2000WO-US004414.
 24-FEB-2000; 2000WO-US004914.
 01-MAR-2000; 2000WO-US005004.
 02-MAR-2000; 2000WO-US005746.
 02-MAR-2000; 2000WO-US005841.
 10-MAR-2000; 2000WO-US006319.
 15-MAR-2000; 2000WO-US006884.
 20-MAR-2000; 2000WO-US007377.
 21-MAR-2000; 2000WO-US007532.
 30-MAR-2000; 2000WO-US008439.
 17-MAY-2000; 2000WO-US013705.
 22-MAY-2000; 2000WO-US014042.
 30-MAY-2000; 2000WO-US014264.
 02-JUN-2000; 2000WO-US015264.
 28-JUL-2000; 2000WO-US020710.
 11-AUG-2000; 2000WO-US022031.
 23-AUG-2000; 2000WO-US023522.
 24-AUG-2000; 2000WO-US023328.
 08-NOV-2000; 2000WO-US030952.
 10-NOV-2000; 2000WO-US030873.
 01-DEC-2000; 2000WO-US032678.
 20-DEC-2000; 2000WO-US034956.
 28-FEB-2001; 2001US-00796498.
 28-FEB-2001; 2001WO-US006520.
 01-MAR-2001; 2001WO-US006666.
 09-MAR-2001; 2001US-00802706.
 14-MAR-2001; 2001US-00808689.
 22-MAR-2001; 2001US-00816744.
 05-APR-2001; 2001US-00828366.
 10-MAY-2001; 2001US-00854208.
 10-MAY-2001; 2001US-00884280.
 18-MAY-2001; 2001US-00860216.
 25-MAY-2001; 2001US-00866028.
 25-MAY-2001; 2001US-00866034.
 25-MAY-2001; 2001WO-US017092.
 01-JUN-2001; 2001US-00872035.
 01-JUN-2001; 2001WO-US017800.
 05-JUN-2001; 2001US-00874503.
 14-JUN-2001; 2001US-00882636.
 19-JUN-2001; 2001US-00886342.
 20-JUN-2001; 2001WO-US019692.
 21-JUN-2001; 2001US-00887879.

22-JUN-2001; 2001WO-US020116.
 29-JUN-2001; 2001WO-US021066.
 09-JUL-2001; 2001WO-US021735.
 18-JUL-2001; 2001US-00908827.
 06-AUG-2001; 2001US-00924419.
 09-AUG-2001; 2001US-00927796.
 16-AUG-2001; 2001US-00931836.
 19-DEC-2001; 2001US-00028072.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;
 XX WPI; 2003-466355/44.
 DR N-PSDB; ACD41887.
 XX
 PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 or
 PT PRO4978, useful in molecular biology, chromosome and gene mapping, in
 PT generating antisense RNA and DNA, and in gene therapy.
 XX
 PS Claim 12; Fig 186; 659pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising at least 80%
 CC sequence identity to a PRO (secreted and transmembrane protein) cDNA
 CC comprising a nucleic acid (a) encoding a PRO polypeptide, or its
 CC extracellular domain (with or without its associated signal peptide),
 CC which comprises any of the 275 120-850 residue amino acid sequences,
 CC given in the specification; (b) comprising any of the 275 300-3500
 CC nucleotide sequences, given in the specification; or (c) comprising the
 CC full-length coding sequence of the nucleotide sequences given in the
 CC specification, or of the DNA deposited under any of the American Type
 CC Culture Collection (ATCC) Accession Numbers listed in the specification.
 CC Also included are a vector comprising the novel nucleic acid, a host cell
 CC comprising the vector, producing a PRO polypeptide, the isolated PRO
 CC polypeptides detailed above, a chimeric molecule comprising the PRO
 CC polypeptide of fused to a heterologous amino acid sequence, an anti-PRO
 CC antibody, detecting a PRO polypeptide in a sample suspected of containing
 CC the PRO polypeptide, linking a bioactive molecule to a cell expressing a
 CC PRO polypeptide, modulating at least one biological activity of a cell
 CC expressing a PRO polypeptide, stimulating the release of tumour necrosis
 CC factor-alpha (TNF-alpha) from human blood, (or proteoglycans from
 CC cartilage or cytokine from peripheral blood mononuclear cells (PBMC)),
 CC modulating the uptake of glucose or FFA by skeletal muscle cells or
 CC adipocyte cells, stimulating the proliferation or differentiation of
 CC chondrocyte cells for proliferation of or gene expression in paricycle
 CC cells, stimulating the proliferation of inner ear utricular supporting
 CC cells (or of T-lymphocyte cells, or of endothelial cells), inhibiting the
 CC binding of A-peptide to factor VIIA, or differentiation of adipocyte
 CC cells, detecting the presence of a tumour in a mammal and an
 CC oligonucleotide probe derived from any of the nucleotide sequences given
 CC in the specification. The polynucleotide is useful in molecular biology,
 CC including uses as hybridisation probes, in chromosome and gene mapping,
 CC in generating antisense RNA and DNA, and in gene therapy. The
 CC polynucleotide may also be used in preparing PRO polypeptides by
 CC recombinant techniques, and in generating either transgenic animals or
 CC knock-out animals which, in turn, are useful in the development and or
 CC screening of therapeutically useful reagents. The PRO polypeptide or the
 CC antibody is used in preparing a medicament for treating a condition
 CC responsive to the polypeptide or antibody, such as tumours, and in
 CC various diagnostic assays. The present sequence represents a PRO
 CC polypeptide
 XX
 SQ Sequence 364 AA;
 Query Match 100.0%; Score 1742; DB 6; Length 364;
 Best Local Similarity 100.0%; Pred. No. 5e-16;
 Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LYRDETIQVKGNGYVQSPFNSYPRNLLTWRLHSQENTRIQLVFDNQGLEAENDI 60
 DB 43 LYRDETIQVKGNGYVQSPFNSYPRNLLTWRLHSQENTRIQLVFDNQGLEAENDI 102

PA (GETH) GENENTECH INC.
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-331925/31.
DR N-PSDB; ACA04116.
XX
XX New secreted and transmembrane nucleic acids and polypeptides, designated
PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,
PT cardiac injury, infertility, birth defects, premature aging, AIDS, or
PT cancer.
XX
XX Claim 12; Fig 186; 659pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising, or which is
CC at least 80% identical to, or the full-length coding sequence of, any of
CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
CC (one of 275 secreted or transmembrane proteins). The nucleic acid further
CC comprises the full-length coding sequence of the DNA deposited under
CC American Type Culture Collection (ATCC) accession number in a list given
CC in the specification. Also included are vectors and host cells for
CC producing PRO proteins, PRO fusion proteins, anti-PRO antibodies, PRO
CC extracellular domains and mature sequences, methods of detecting PRO
CC proteins, methods for stimulating the release of TNF-alpha (tumour
CC necrosis factor alpha) from human blood, (and the proliferation of
CC differentiation of chondrocyte cells, the proliferation of, or gene
CC expression in pericyte cells, the release or proteoglycans from
CC cartilage, proliferation of inner ear utricular supporting cells, the
CC proliferation of T-lymphocyte cells, the release of a cytokine from
CC peripheral blood mononuclear cells (PBMC), or the proliferation of
CC endothelial cells), a method for modulating the uptake of glucose or free
CC fatty acid (FFA) by skeletal muscle cells, a method for inhibiting the
CC binding of A-peptide to factor VIIA, or the differentiation of adipocyte
CC cells, a method for detecting the presence of a tumour in a mammal and an
CC oligonucleotide probe derived from any of the nucleotide sequences cited
CC above. The nucleic acids and polypeptides are useful for treating
CC inflammatory diseases, organ failure, atherosclerosis, cardiac injury,
CC infertility, birth defects, premature aging, AIDS (acquired
CC immunodeficiency syndrome), cancer, or diabetic complications. The
CC nucleic acids are useful as hybridisation probes, in chromosome and gene
CC mapping, and in generating antisense RNA or DNA. The polypeptides are
CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both
CC are useful in tissue typing. The present sequence represents a PRO
CC protein of the invention
XX
XX Sequence 364 AA;
S

Query Match 100.0%; Score 1742; DB 6; Length 364;
Best Local Similarity 100.0%; Pred. No. 5e-166;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LYRRDETIOVKGNGYVQSPFRFNSYPRNLLLTWRHLSQENTRIQLVFNQFGLAEANDI 60
DB 43 LYRRDETIOVKGNGYVQSPFRFNSYPRNLLLTWRHLSQENTRIQLVFNQFGLAEANDI 102
QY 61 CRYDFVEVEDISGTSTIIRGRCGHEKVPPIKSRNTQIKITFKSDDYFVAKPGFKIYYS 120
DB 103 CRYDFVEVEDISGTSTIIRGRCGHEKVPPIKSRNTQIKITFKSDDYFVAKPGFKIYYS 162
QY 121 LLEDQPAASATNWSVTSSISGVSYNSPSTVDPTLIADALDKKIAEFTVVDLLKYFN 180
DB 163 LLEDQPAASATNWSVTSSISGVSYNSPSTVDPTLIADALDKKIAEFTVVDLLKYFN 222
QY 181 PESWQEDLENMYLDTPRYGRSHDRKSKVDLDRDLNDKAKRYSCTPRNSYNIREELKLA 240
DB 223 PESWQEDLENMYLDTPRYGRSHDRKSKVDLDRDLNDKAKRYSCTPRNSYNIREELKLA 282
QY 241 NVVFFPRCLLVQRCGNGCCGVVNRSCITCNSGKTVKKYHEVLQEPGHIKRRGAKTWA 300
DB 283 NVVFFPRCLLVQRCGNGCCGVVNRSCITCNSGKTVKKYHEVLQEPGHIKRRGAKTWA 342

QY 301 LVDIQLDHHRCDCICSSRPPR 322
DB 343 LVDIQLDHHRCDCICSSRPPR 364
RESULT 13
ADA45705
ID ADA45705 standard; protein; 364 AA.
XX
XX AC ADA45705;
XX DT 20-NOV-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO4345.
XX KW Human; secreted and transmembrane protein; PRO;
KW Tumour necrosis factor alpha release; TNF-alpha release;
KW glucose uptake modulator; FFA uptake modulator;
KW cell proliferation stimulator; cell differentiation stimulator;
KW cell differentiation inhibitor; cytokine release stimulator; tumour;
KW lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour;
KW cervical tumour; liver tumour; chromosome mapping; gene mapping;
KW gene therapy; chromosome identification; chromosome marker.
XX OS Homo sapiens.
XX PN US2003022328-A1.
XX PD 30-JAN-2003.
XX PF 16-APR-2002; 2002US-00123904.
XX PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031244.

PR	05-JAN-2000;	2000WO-US000219.
PR	06-JAN-2000;	2000WO-US000277.
PR	06-JAN-2000;	2000WO-US000376.
PR	11-FEB-2000;	2000WO-US000365.
PR	18-FEB-2000;	2000WO-US004341.
PR	18-FEB-2000;	2000WO-US004342.
PR	22-FEB-2000;	2000WO-US004414.
PR	24-FEB-2000;	2000WO-US004914.
PR	24-FEB-2000;	2000WO-US005004.
PR	01-MAR-2000;	2000WO-US005601.
PR	02-MAR-2000;	2000WO-US005746.
PR	02-MAR-2000;	2000WO-US005841.
PR	10-MAR-2000;	2000WO-US006319.
PR	15-MAR-2000;	2000WO-US006884.
PR	20-MAR-2000;	2000WO-US007377.
PR	21-MAR-2000;	2000WO-US007532.
PR	30-MAR-2000;	2000WO-US008439.
PR	17-MAY-2000;	2000WO-US013705.
PR	22-MAY-2000;	2000WO-US014042.
PR	30-MAY-2000;	2000WO-US014941.
PR	02-JUN-2000;	2000WO-US015264.
PR	28-JUL-2000;	2000WO-US020710.
PR	11-AUG-2000;	2000WO-US022031.
PR	23-AUG-2000;	2000WO-US023522.
PR	24-AUG-2000;	2000WO-US023328.
PR	08-NOV-2000;	2000WO-US030952.
PR	10-NOV-2000;	2000WO-US030873.
PR	01-DEC-2000;	2000WO-US032678.
PR	20-DEC-2000;	2000US-00747259.
PR	20-DEC-2000;	2000WO-US034956.
PR	28-FEB-2001;	2000US-00796498.
PR	28-FEB-2001;	2001WO-US006520.
PR	01-MAR-2001;	2001WO-US006666.
PR	09-MAR-2001;	2001US-00802706.
PR	14-MAR-2001;	2001US-00808689.
PR	22-MAR-2001;	2001US-00816744.
PR	05-APR-2001;	2001US-00828366.
PR	10-MAY-2001;	2001US-00854208.
PR	10-MAY-2001;	2001US-00854280.
PR	18-MAY-2001;	2001US-00860216.
PR	25-MAY-2001;	2001US-00866028.
PR	25-MAY-2001;	2001US-00866034.
PR	25-MAY-2001;	2001WO-US017092.
PR	01-JUN-2001;	2001US-00872035.
PR	01-JUN-2001;	2001WO-US017800.
PR	05-JUN-2001;	2001US-00874503.
PR	14-JUN-2001;	2001US-00882636.
PR	19-JUN-2001;	2001US-00886342.
PR	20-JUN-2001;	2001WO-US019692.
PR	21-JUN-2001;	2001US-00887879.
PR	22-JUN-2001;	2001WO-US020116.
PR	29-JUN-2001;	2001WO-US021066.
PR	09-JUL-2001;	2001WO-US021735.
PR	18-JUL-2001;	2001US-00908827.
PR	06-AUG-2001;	2001US-00924419.
PR	09-AUG-2001;	2001US-00927796.
PR	16-AUG-2001;	2001US-00931836.
PR	19-DEC-2001;	2001US-00028072.
XX		
XX	(GETH)	GENENTECH INC.
XX		
PI	Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;	
PI	Gerlitsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;	
PI	Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;	
XX		
DR	WPI; 2003-584997/55.	
DR	N-PSDB; ADA45704.	
XX		
PT	Novel secreted and transmembrane polypeptide for modulating biological	
PT	activity of cell expressing the polypeptide, identifying agonists or	
PT	antagonists of polypeptide, and as molecular weight markers.	
XX		
XX	Claim 12; Fig 186; 659pp; English.	

The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (I). (I) is useful for stimulating the release of TNF-alpha from human blood, for modulating the uptake of glucose or FFA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the release of proteoglycans from cartilage, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the release of a cytokine from BMC cells, for inhibiting the binding of A-peptide to factor VIIa, for inhibiting the differentiation of adipocyte cells, for stimulating proliferation of endothelial cells, for detecting the presence of tumour in a mammal. The tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour. The oligonucleotide probes are useful for isolating genomic and cDNA nucleotide sequences or antisense probes. (II) is also useful as therapeutic agent. PRO is useful in assays to identify other proteins or molecules involved in binding interaction. A polynucleotide (II) encoding (I) is useful in chromosome CC and gene mapping, in generation of antisense RNA and DNA, in the CC preparation of PRO polypeptide, for generating transgenic animals or CC knockout animals which in turn are useful in the development and CC screening of therapeutically useful reagents, in gene therapy, for CC chromosome identification, as chromosome marker, and for generating CC probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g. CC detecting its expression in specific cells, tissues or serum, and for CC affinity purification of PRO from recombinant cell culture or natural CC sources. (I) and (II) are useful for tissue typing. This is the amino CC acid sequence of a novel human secreted and transmembrane PRO CC polypeptide.

Query Match 100.0%; Score 1742; DB 6; Length 364;
 Best Local Similarity 100.0%; Pred. No. 5e-166;
 Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy	1	LYRDETIQVKGNGYVQSPFPNSYPRLNLLTWRLHSQENTRIQLVFDNQFGLAEAENDI	60
Db	43	LYRDETIQVKGNGYVQSPFPNSYPRLNLLTWRLHSQENTRIQLVFDNQFGLAEAENDI	102
Qy	61	CRYDFVEVEDISETSTIIRGRWCCHKVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS	120
Db	103	CRYDFVEVEDISETSTIIRGRWCCHKVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS	162
Qy	121	LLEDQFPAASSETNWESVTSSISGVSYNSPSVPTPTLIADALDKKIAEFDTVEDLLKYFN	180
Db	163	LLEDQFPAASSETNWESVTSSISGVSYNSPSVPTPTLIADALDKKIAEFDTVEDLLKYFN	222
Qy	181	PESWQEDLENNYLDTPRYGRSYHDRKSKVDLDRLNDDAKRYSCTPRNSYVNIREEKLA	240
Db	223	PESWQEDLENNYLDTPRYGRSYHDRKSKVDLDRLNDDAKRYSCTPRNSYVNIREEKLA	282
Qy	241	NVVFPPRCLLVQRCGNGCGGTWNWRSCTCNISGKTVKKYHVLQEPGHHIKRGRAKTMA	300
Db	283	NVVFPPRCLELVQRCGNGCGGTWNWRSCTCNISGKTVKKYHVLQEPGHHIKRGRAKTMA	342
Qy	301	LVDIQLDHHERCDCICSSRPFR 322	
Db	343	LVDIQLDHHERCDCICSSRPFR 364	

RESULT 14
 ADA761136
 ID ADA761136 standard; protein; 364 AA.
 XX ADA761136;
 XX
 XX 20-NOV-2003 (first entry)
 DT
 XX Human PRO polypeptide #93.
 DE
 XX Human; PRO; secreted polypeptide; transmembrane polypeptide;
 KW

KW	tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour;	20-MAR-2000; 2000WO-US007377.	PR
KW	cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix;	21-MAR-2000; 2000WO-US007532.	PR
KW	liver; microvascular endothelial cell; glucose; FFA;	30-MAR-2000; 2000WO-US008439.	PR
KW	skeletal muscle cell; adipocyte cell; pericyte cell;	17-MAY-2000; 2000WO-US013705.	PR
KW	inner ear utricular supporting cell; T-lymphocyte cell;	22-MAY-2000; 2000WO-US014042.	PR
KW	endothelial cell tube formation; bone disorder; cartilage disorder;	30-MAY-2000; 2000WO-US014941.	PR
KW	sports injury; proteoglycan; articular cartilage defect; osteoarthritis;	02-JUN-2000; 2000WO-US015264.	PR
KW	rheumatoid arthritis; hemoglobin-associated disorder thalassaemia;	28-JUL-2000; 2000WO-US020710.	PR
KW	immune system cell infiltration.	11-AUG-2000; 2000WO-US022031.	PR
XX		23-AUG-2000; 2000WO-US023522.	PR
OS	Homo sapiens.	24-AUG-2000; 2000WO-US023328.	PR
XX		08-NOV-2000; 2000WO-US030952.	PR
PN	US2003073212-A1.	10-NOV-2000; 2000WO-US030873.	PR
XX		01-DEC-2000; 2000WO-US032678.	PR
PD		20-DEC-2000; 2000US-00747259.	PR
XX		20-DEC-2000; 2000WO-US034956.	PR
PF		28-FEB-2001; 2001US-00796498.	PR
XX		28-FEB-2001; 2001WO-US006520.	PR
PF		01-MAR-2001; 2001WO-US006666.	PR
XX		09-MAR-2001; 2001US-00802706.	PR
XX		14-MAR-2001; 2001US-00808689.	PR
XX		22-MAR-2001; 2001US-00816744.	PR
XX		05-APR-2001; 2001US-00828366.	PR
XX		10-MAY-2001; 2001US-00854208.	PR
XX		10-MAY-2001; 2001US-00854280.	PR
XX		18-MAY-2001; 2001US-00860216.	PR
XX		25-MAY-2001; 2001US-00866034.	PR
XX		25-MAY-2001; 2001WO-US017092.	PR
XX		01-JUN-2001; 2001US-00872035.	PR
XX		01-JUN-2001; 2001WO-US017800.	PR
XX		05-JUN-2001; 2001US-00874503.	PR
XX		14-JUN-2001; 2001US-00882636.	PR
XX		19-JUN-2001; 2001US-00886342.	PR
XX		20-JUN-2001; 2001WO-US019692.	PR
XX		21-JUN-2001; 2001US-00887879.	PR
XX		22-JUN-2001; 2001WO-US020116.	PR
XX		29-JUN-2001; 2001WO-US021066.	PR
XX		09-JUL-2001; 2001WO-US021735.	PR
XX		18-JUL-2001; 2001US-00908827.	PR
XX		06-AUG-2001; 2001US-00924419.	PR
XX		09-AUG-2001; 2001US-00927796.	PR
XX		16-AUG-2001; 2001US-00931836.	PR
XX		19-DEC-2001; 2001US-00028072.	PR
XX			XX
XX		(GETH) GENENTECH INC.	XX
XX		Baker KP; Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;	XX
PI	Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;		PI
PI	Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;		PI
XX	WPI; 2003-687639/65.		XX
DR	N-PSDB; ADA76135.		DR
XX			XX
PT	New isolated nucleic acid encoding a secreted and transmembrane		PT
PT	polypeptide, designated e.g. PRO1114 or PRO4978, useful in chromosome and		PT
PT	gene mapping, in generating antisense RNA and DNA, and in gene therapy.		PT
XX	Claim 12; Fig 186; 659pp; English.		XX
XX			XX
CC	The invention relates to isolated human PRO polypeptides (secreted and		CC
CC	transmembrane polypeptides) and the polynucleotides encoding them. The		CC
CC	invention also relates to an antibody which specifically binds to a PRO		CC
CC	polypeptide, a method for stimulating the release of tumour necrosis		CC
CC	factor-alpha (TNF-alpha) from human blood, a method for stimulating the		CC
CC	proliferation or differentiation of chondrocyte cells and a method for		CC
CC	detecting the presence of a tumour in a mammal (e.g. adrenal, lung,		CC
CC	colon, breast, prostate, rectal, kidney, cervical and liver tumours) . The		CC
CC	polynucleotides are useful in molecular biology, including uses as		CC
CC	hybridisation probes, in chromosome and gene mapping, in generating		CC
CC	antisense RNA and DNA and in gene therapy. The polynucleotides may also		CC
CC	be used in preparing PRO polypeptides by recombinant techniques and in		CC
CC	generating either transgenic animals or knock-out animals which are		CC

useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for modulating the uptake of glucose or FFA by skeletal muscle cells or adipocyte cells, for stimulating differentiation of adipocyte cells, for stimulating proliferation of gene expression in pericyte cells, for stimulating the proliferation of inner ear utricular supporting cells or T-lymphocyte cells, for inducing endothelial cell tube formation and for treating various bone and/or cartilage disorders such as sports injuries and arthritis. PRO polypeptides which stimulate the release of proteoglycans from cartilage are useful for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful for treating various mammalian haemoglobin-associated disorders such as various thalassaemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human PRO polypeptide of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

20-DEC-2000; 2000US-00747259.
20-DEC-2000; 2000WO-US034956.
28-FEB-2001; 2001US-00796498.
28-FEB-2001; 2001WO-US006520.
01-MAR-2001; 2001WO-US006666.
09-MAR-2001; 2001US-00802706.
14-MAR-2001; 2001US-00808689.
22-MAR-2001; 2001US-00816744.
05-APR-2001; 2001US-00828366.
10-MAY-2001; 2001US-00854208.
18-MAY-2001; 2001US-00860216.
25-MAY-2001; 2001US-00866028.
25-MAY-2001; 2001US-00866034.
25-MAY-2001; 2001WO-US017092.
01-JUN-2001; 2001US-00872035.
01-JUN-2001; 2001WO-US017800.
05-JUN-2001; 2001US-00874503.
14-JUN-2001; 2001US-00882636.
19-JUN-2001; 2001US-00886342.
20-JUN-2001; 2001WO-US019692.
21-JUN-2001; 2001US-00887879.
22-JUN-2001; 2001WO-US020116.
29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
18-JUL-2001; 2001US-00908827.
06-AUG-2001; 2001US-00924419.
09-AUG-2001; 2001US-00927796.
16-AUG-2001; 2001US-00931836.
19-DEC-2001; 2001US-00028072.
XX
PA (GETH) GENENTECH INC.
XX
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-521854/49.
DR N-PSDB; ADA18785.
XX
XX New PRO nucleic acid, useful for preparing a composition for treating
PT e.g., tumors.
XX
XX Claim 12; Fig 186; 660pp; English.
XX
CC The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,
CC prostate, rectal, cervical and liver tumours). The polynucleotides are
CC useful in molecular biology, including uses as hybridisation probes, in
CC chromosome and gene mapping, in generating antisense RNA and DNA and in
CC gene therapy. The polynucleotides may also be used in preparing PRO
CC polypeptides by recombinant techniques and in generating either
CC transgenic animals or knock-out animals which are useful in the
CC development and screening of therapeutically useful reagents. The PRO
CC polypeptides or antibodies are used in preparing a medicament for
CC treating a condition responsive to the polypeptides or antibodies, such
CC as tumours, for modulating the uptake of glucose or FFA by adipocyte
CC cells, for stimulating the proliferation of or gene expression in
CC priocyte cells, for stimulating the release of proteoglycans from
CC cartilage, for stimulating the proliferation of inner ear utricular
CC supporting cells, for stimulating the release of cytokines from PBMC
CC cells, for inhibiting the binding of A-peptide to factor VIIa, for
CC inhibiting the differentiation of adipocyte cells and for stimulating the
CC proliferation of endothelial cells. This sequence represents a human PRO
CC polypeptide of the invention. Note: The sequence data for this patent is
CC also available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX

SQ Sequence 364 AA;		Query Match		100.0%; Score 1742; DB 6; Length 364;	
		Best Local Similarity		100.0%; Pred. No. 5e-166;	
Matches 322; Conservative		0; Mismatches		0; Indels	
		0; Gaps		0;	
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Db	43	LYRDETIQVKGNGYVQSPFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLAEAE	DI	102	
QY	61	CRYDFVEVEDISSTTIIRGRWCGHKVPPRIKSRTNQIKITPKSDDYFVAKPGFKI	YS	120	
Db	103	CRYDFVEVEDISSTTIIRGRWCGHKVPPRIKSRTNQIKITPKSDDYFVAKPGFKI	YS	162	
QY	121	LLEDFOPAASSETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTDVEDLL	KYFN	180	
Db	163	LLEDFOPAASSETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTDVEDLL	KYFN	222	
QY	181	PESWQEDLENMYLDTPIRYGRKSYHDKRSKYVDLRLNDDAKRYSCTPRNYSVNIREEL	KLA	240	
Db	223	PESWQEDLENMYLDTPIRYGRKSYHDKRSKYVDLRLNDDAKRYSCTPRNYSVNIREEL	KLA	282	
QY	241	NVFFPRCLLVORCGNGCGCTVNRSCCTNSGKTVKKYHEVLQFEPGHIKRGRAKTMA	300		
Db	283	NVFFPRCLLVORCGNGCGCTVNRSCCTNSGKTVKKYHEVLQFEPGHIKRGRAKTMA	342		
QY	301	LVDIQLDHHERCDCICSSRPPR	322		
Db	343	LVDIQLDHHERCDCICSSRPPR	364		

Search completed: October 29, 2004, 23:29:11
Job time : 164 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 29, 2004, 23:24:15 ; Search time 39 Seconds
(without alignments)
547.549 Million cell updates/sec

Title: US-10-086-623-6

Perfect score: 1742

Sequence: 1 LYRDETQVKGNGYVQSPR.....DIQLDHERCUCICSSRPPR 322

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents_AA.*
- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1742	100.0	322	4	US-09-438-046-6
2	1742	100.0	364	4	US-10-140-002-186
3	1742	100.0	370	4	US-09-457-066-37
4	1742	100.0	370	4	US-09-540-224-2
5	1742	100.0	370	4	US-09-564-595D-2
6	1742	100.0	370	4	US-09-706-968-37
7	1742	100.0	370	4	US-09-808-972-2
8	1742	100.0	370	4	US-09-823-033-5
9	1742	100.0	370	4	US-09-438-046-8
10	1561	89.6	370	4	US-09-564-595D-53
11	1561	89.6	370	4	US-09-808-972-4
12	1561	89.6	370	4	US-09-564-595D-56
13	1403	80.5	317	4	US-09-564-595D-54
14	1357.5	77.9	316	4	US-09-564-595D-55
15	1095	62.9	303	4	US-09-564-595D-57
16	1061.5	60.9	302	4	US-09-564-595D-54
17	982	56.4	200	4	US-09-438-046-4
18	750.5	43.1	345	4	US-09-457-066-43
19	750.5	43.1	345	4	US-09-564-595D-35
20	750.5	43.1	345	4	US-09-706-968-43
21	750.5	43.1	345	4	US-09-823-033-4
22	739.5	42.5	323	4	US-09-468-647-1
23	739.5	42.5	345	3	US-09-040-220D-2
24	739.5	42.5	345	4	US-09-457-066-2
25	739.5	42.5	345	4	US-09-265-686-2
26	739.5	42.5	345	4	US-09-540-224-5
27	739.5	42.5	345	4	US-09-564-595D-33

28	739.5	42.5	345	4	US-09-706-968-2	Sequence 2, Appli
29	739.5	42.5	345	4	US-09-723-749-2	Sequence 2, Appli
30	739.5	42.5	345	4	US-09-823-033-2	Sequence 2, Appli
31	739.5	42.5	345	4	US-10-140-002-286	Sequence 286, App
32	739.5	42.5	345	4	US-09-468-647-2	Sequence 2, Appli
33	651	37.4	121	4	US-09-438-046-18	Sequence 18, Appl
34	637	36.6	119	4	US-09-438-046-19	Sequence 19, Appl
35	380	21.8	66	4	US-09-438-046-2	Sequence 2, Appli
36	329.5	18.9	132	4	US-09-468-647-29	Sequence 29, Appl
37	328.5	18.9	168	4	US-09-468-647-27	Sequence 27, Appl
38	295.5	17.0	111	4	US-09-468-647-26	Sequence 26, Appl
39	187.5	10.8	788	1	US-08-572-225-1	Sequence 1, Appli
40	187.5	10.8	986	4	US-09-285-385C-19	Sequence 19, Appl
41	186.5	10.7	730	3	US-08-872-757-2	Sequence 2, Appli
42	186.5	10.7	730	4	US-09-850-048A-2	Sequence 2, Appli
43	186.5	10.7	1015	4	US-09-285-385C-2	Sequence 2, Appli
44	183.5	10.5	1012	4	US-09-285-385C-4	Sequence 4, Appli
45	180.5	10.4	101	3	US-09-374-135-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-438-046-6
; Sequence 6, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTN, Annica
; APPLICANT: UTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
; FILE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; CURRENT FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; EARLIER FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-438-046-6

Query Match	100.0%;	Score 1742;	DB 4;	Length 322;
Best Local Similarity	100.0%;	Pred. No. 1.4e-172;	Indels 0;	Gaps 0;
Matches 322;	Conservative	0;	Mismatches	0;
QY	1	LYRDETQVKGNGYVQSPRPNNSYPRNLLTWRLHSEOENTRIQLVFNQFGLERAENDI	60	
Db	1	LYRDETQVKGNGYVQSPRPNNSYPRNLLTWRLHSEOENTRIQLVFNQFGLERAENDI	60	
QY	61	CRYDFEVEDISETSTIIRGRWCCHKEVPPRIKSTNQIKITFKSDDYFVAKPGFKIYVS	120	
Db	61	CRYDFEVEDISETSTIIRGRWCCHKEVPPRIKSTNQIKITFKSDDYFVAKPGFKIYVS	120	
QY	121	LLEDQPPAAASSETNWESVTSSISGVSYNSPSTDTLTADALDKKIAEDTVDLLKYN	180	

Db 121 LLEDFOAAAASETNNWESVTSISGVSYNSPSTVDTPTLIADALDKKIAEFTVTELLKYFN 180
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Db 181 PESWQEDLENMYLDTPRYGRSHYDRKSKVDLRLNDLNDKRYSCPTPRNYSVNIREEKLA 240
QY 241 NVVFFPRCLLVORCGNCGCGTVNWRSCVTSNKGKTVKKYHEVLQPEPGHKKRGRAKTMA 300
Db 241 NVVFFPRCLLVORCGNCGCGTVNWRSCVTSNKGKTVKKYHEVLQPEPGHKKRGRAKTMA 300
QY 301 LVDIQLDHHERCDCICSSRPPR 322
Db 301 LVDIQLDHHERCDCICSSRPPR 322

RESULT 2

US-10-140-002-186
; Sequence 186, Application US/10140002
; Patent No. 6725730

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RJC59
; CURRENT APPLICATION NUMBER: US/10/140,002
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 186
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo Sapien

US-10-140-002-186

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Best Local Similarity 100.0%; Pred. No. 1.7e-172; Indels 0; Gaps 0;
Matches 322; Conservative 0; Mismatches 0;

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Db 103 CRYDFVEVEDISSETTIIRGRCGHEVPPIKSRNTQIKITFKSDDYFVAKPGPKIYYS 162
QY 121 LLEDFOAAAASETNNWESVTSISGVSYNSPSTVDTPTLIADALDKKIAEFTVTELLKYFN 180
Db 163 LLEDFOAAAASETNNWESVTSISGVSYNSPSTVDTPTLIADALDKKIAEFTVTELLKYFN 222
QY 181 PESWQEDLENMYLDTPRYGRSHYDRKSKVDLRLNDLNDKRYSCPTPRNYSVNIREEKLA 240
Db 223 PESWQEDLENMYLDTPRYGRSHYDRKSKVDLRLNDLNDKRYSCPTPRNYSVNIREEKLA 282
QY 241 NVVFFPRCLLVORCGNCGCGTVNWRSCVTSNKGKTVKKYHEVLQPEPGHKKRGRAKTMA 300
Db 283 NVVFFPRCLLVORCGNCGCGTVNWRSCVTSNKGKTVKKYHEVLQPEPGHKKRGRAKTMA 342

QY 301 LVDIQLDHHERCDCICSSRPPR 322
Db 343 LVDIQLDHHERCDCICSSRPPR 364

RESULT 3

US-09-457-066-37
; Sequence 37, Application US/09457066
; Patent No. 6432673

GENERAL INFORMATION:

; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3

; FILE REFERENCE: 98-60

; CURRENT APPLICATION NUMBER: US/09/457,066

; CURRENT FILING DATE: 1999-12-07

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 37

; LENGTH: 370

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-457-066-37

Query Match 100.0%; Score 1742; DB 4; Length 370;

Best Local Similarity 100.0%; Pred. No. 1.8e-172;

Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LYRDETIQVKGNGYVQSPFPNSYPRNLLTWRLHSEOENTRIQLVFNQFGLBEAENDI 60
Db 49 LYRDETIQVKGNGYVQSPFPNSYPRNLLTWRLHSEOENTRIQLVFNQFGLBEAENDI 108
QY 61 CRYDFVEVEDISSETTIIRGRCGHEVPPIKSRNTQIKITFKSDDYFVAKPGPKIYYS 120
Db 109 CRYDFVEVEDISSETTIIRGRCGHEVPPIKSRNTQIKITFKSDDYFVAKPGPKIYYS 168
QY 121 LLEDFOAAAASETNNWESVTSISGVSYNSPSTVDTPTLIADALDKKIAEFTVTELLKYFN 180
Db 169 LLEDFOAAAASETNNWESVTSISGVSYNSPSTVDTPTLIADALDKKIAEFTVTELLKYFN 228
QY 181 PESWQEDLENMYLDTPRYGRSHYDRKSKVDLRLNDLNDKRYSCPTPRNYSVNIREEKLA 240
Db 229 PESWQEDLENMYLDTPRYGRSHYDRKSKVDLRLNDLNDKRYSCPTPRNYSVNIREEKLA 283
QY 241 NVVFFPRCLLVORCGNCGCGTVNWRSCVTSNKGKTVKKYHEVLQPEPGHKKRGRAKTMA 300
Db 289 NVVFFPRCLLVORCGNCGCGTVNWRSCVTSNKGKTVKKYHEVLQPEPGHKKRGRAKTMA 348
QY 301 LVDIQLDHHERCDCICSSRPPR 322
Db 349 LVDIQLDHHERCDCICSSRPPR 370

RESULT 4

US-09-540-224-2
; Sequence 2, Application US/09540224
; Patent No. 6468543

GENERAL INFORMATION:

; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04

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; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-540-224-2

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Best Local Similarity 100.0%; Pred. No. 1.8e-172;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LYRDETIQVKGNGYVQSPRPNSYPRLNLLTWLHSEOENTRIQLVFNQFGLSEAENDI 60
Db 49 LYRDETIQVKGNGYVQSPRPNSYPRLNLLTWLHSEOENTRIQLVFNQFGLSEAENDI 108
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Db 109 CRYDFVEVEDISSETTIIRGWCHEKVPPIKSRITQIKITFKSDDYFVAKPGFKIYYS 168
Qy 121 LLEDQFAAAASSETNWESVTSSISGVSYNSPSVPTDPTLIADALDKKIAEFDTVEDLLKYFN 180
Db 169 LLEDQFAAAASSETNWESVTSSISGVSYNSPSVPTDPTLIADALDKKIAEFDTVEDLLKYFN 228
Qy 181 PESQEDLENNYLDTPRYGRSYHDKRSKVDLRLNDDAKRYSCCTPRNYSVNIIEELKLA 240
Db 229 PESQEDLENNYLDTPRYGRSYHDKRSKVDLRLNDDAKRYSCCTPRNYSVNIIEELKLA 288
Qy 241 NVVFPFRCLLVQRCGCGCGCTVNWRSCTCNSGKTVKHYHEVLOFEPGHIKRRGRAKTM 300
Db 289 NVVFPFRCLLVQRCGCGCGCTVNWRSCTCNSGKTVKHYHEVLOFEPGHIKRRGRAKTM 348
Qy 301 LVDIQLDHERCDCICSSRPPR 322
Db 349 LVDIQLDHERCDCICSSRPPR 370

RESULT 5
US-09-564-5950-2
; Sequence 2, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-564-595D-2

Query Match      100.0%; Score 1742; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.8e-172;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LYRDETIQVKGNGYVQSPRPNSYPRLNLLTWLHSEOENTRIQLVFNQFGLSEAENDI 60
Db 49 LYRDETIQVKGNGYVQSPRPNSYPRLNLLTWLHSEOENTRIQLVFNQFGLSEAENDI 108
Qy 61 CRYDFVEVEDISSETTIIRGWCHEKVPPIKSRITQIKITFKSDDYFVAKPGFKIYYS 120
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Db 109 CRYDFVEVEDISSETTIIRGWCHEKVPPIKSRITQIKITFKSDDYFVAKPGFKIYYS 168
Qy 121 LLEDQFAAAASSETNWESVTSSISGVSYNSPSVPTDPTLIADALDKKIAEFDTVEDLLKYFN 180
Db 169 LLEDQFAAAASSETNWESVTSSISGVSYNSPSVPTDPTLIADALDKKIAEFDTVEDLLKYFN 228
Qy 181 PESQEDLENNYLDTPRYGRSYHDKRSKVDLRLNDDAKRYSCCTPRNYSVNIIEELKLA 240
Db 229 PESQEDLENNYLDTPRYGRSYHDKRSKVDLRLNDDAKRYSCCTPRNYSVNIIEELKLA 288
Qy 241 NVVFPFRCLLVQRCGCGCGCTVNWRSCTCNSGKTVKHYHEVLOFEPGHIKRRGRAKTM 300
Db 289 NVVFPFRCLLVQRCGCGCGCTVNWRSCTCNSGKTVKHYHEVLOFEPGHIKRRGRAKTM 348
Qy 301 LVDIQLDHERCDCICSSRPPR 322
Db 349 LVDIQLDHERCDCICSSRPPR 370

RESULT 6
US-09-706-968-37
; Sequence 37, Application US/09706968
; Patent No. 6528050
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60C1
; CURRENT APPLICATION NUMBER: US/09/706,968
; CURRENT FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: US/09/541,752
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-706-968-37

Query Match      100.0%; Score 1742; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.8e-172;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LYRDETIQVKGNGYVQSPRPNSYPRLNLLTWLHSEOENTRIQLVFNQFGLSEAENDI 60
Db 49 LYRDETIQVKGNGYVQSPRPNSYPRLNLLTWLHSEOENTRIQLVFNQFGLSEAENDI 108
Qy 61 CRYDFVEVEDISSETTIIRGWCHEKVPPIKSRITQIKITFKSDDYFVAKPGFKIYYS 120
Db 109 CRYDFVEVEDISSETTIIRGWCHEKVPPIKSRITQIKITFKSDDYFVAKPGFKIYYS 168
Qy 121 LLEDQFAAAASSETNWESVTSSISGVSYNSPSVPTDPTLIADALDKKIAEFDTVEDLLKYFN 180
Db 169 LLEDQFAAAASSETNWESVTSSISGVSYNSPSVPTDPTLIADALDKKIAEFDTVEDLLKYFN 228
Qy 181 PESQEDLENNYLDTPRYGRSYHDKRSKVDLRLNDDAKRYSCCTPRNYSVNIIEELKLA 240
Db 229 PESQEDLENNYLDTPRYGRSYHDKRSKVDLRLNDDAKRYSCCTPRNYSVNIIEELKLA 288
Qy 241 NVVFPFRCLLVQRCGCGCGCTVNWRSCTCNSGKTVKHYHEVLOFEPGHIKRRGRAKTM 300
Db 289 NVVFPFRCLLVQRCGCGCGCTVNWRSCTCNSGKTVKHYHEVLOFEPGHIKRRGRAKTM 348
Qy 301 LVDIQLDHERCDCICSSRPPR 322
Db 349 LVDIQLDHERCDCICSSRPPR 370
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RESULT 7
US-09-808-972-2
; Sequence 2, Application US/09808972
; Patent No. 6630142
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 00-79
; CURRENT APPLICATION NUMBER: US/09/808,972
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/235,295
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/132,250
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-972-2

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```

Query Match      100.0%; Score 1742; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.8e-172;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LYRDETIQVKGNGYVQSPRPNSYPNLLLTWRLHSEQENTRIQLVFNQFGLAEANDI 60
Db 49 LYRDETIQVKGNGYVQSPRPNSYPNLLLTWRLHSEQENTRIQLVFNQFGLAEANDI 108
QY 61 CRYDFEVEVEDISSETIIRGRWCGHKEVPRIKSRNQIKITFKSDDYFVAKPGFKIYYS 120
Db 109 CRYDFEVEVEDISSETIIRGRWCGHKEVPRIKSRNQIKITFKSDDYFVAKPGFKIYYS 168
QY 121 LLEDFOPAASSETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVDELLKYFN 180
Db 169 LLEDFOPAASSETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVDELLKYFN 228
QY 181 PESWQEDLENNMYLDTPRYGRSYHDKRSKVLDRLNDLNDKAKRYSCCTPRNYSVNIREEKLA 240
Db 229 PESWQEDLENNMYLDTPRYGRSYHDKRSKVLDRLNDLNDKAKRYSCCTPRNYSVNIREEKLA 288
QY 241 NVVFFPRCLLVQRCGNGCGGTVNWRSCNCGTKVKKYHEVLQFEPGHIKRRGRAKTMA 300
Db 289 NVVFFPRCLLVQRCGNGCGGTVNWRSCNCGTKVKKYHEVLQFEPGHIKRRGRAKTMA 348
QY 301 LVDIQLDHHRCDCICSSRPPR 322
Db 349 LVDIQLDHHRCDCICSSRPPR 370

```

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RESULT 8
US-09-823-033-5
; Sequence 5, Application US/09823033
; Patent No. 6663870
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/09/823,033
; CURRENT FILING DATE: 2001-03-29

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; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-823-033-5

Query Match      100.0%; Score 1742; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.8e-172;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LYRDETIQVKGNGYVQSPRPNSYPNLLLTWRLHSEQENTRIQLVFNQFGLAEANDI 60
Db 49 LYRDETIQVKGNGYVQSPRPNSYPNLLLTWRLHSEQENTRIQLVFNQFGLAEANDI 108
QY 61 CRYDFEVEVEDISSETIIRGRWCGHKEVPRIKSRNQIKITFKSDDYFVAKPGFKIYYS 120
Db 109 CRYDFEVEVEDISSETIIRGRWCGHKEVPRIKSRNQIKITFKSDDYFVAKPGFKIYYS 168
QY 121 LLEDFOPAASSETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVDELLKYFN 180
Db 169 LLEDFOPAASSETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVDELLKYFN 228
QY 181 PESWQEDLENNMYLDTPRYGRSYHDKRSKVLDRLNDLNDKAKRYSCCTPRNYSVNIREEKLA 240
Db 229 PESWQEDLENNMYLDTPRYGRSYHDKRSKVLDRLNDLNDKAKRYSCCTPRNYSVNIREEKLA 288
QY 241 NVVFFPRCLLVQRCGNGCGGTVNWRSCNCGTKVKKYHEVLQFEPGHIKRRGRAKTMA 300
Db 289 NVVFFPRCLLVQRCGNGCGGTVNWRSCNCGTKVKKYHEVLQFEPGHIKRRGRAKTMA 348
QY 301 LVDIQLDHHRCDCICSSRPPR 322
Db 349 LVDIQLDHHRCDCICSSRPPR 370

```

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RESULT 9
US-09-438-046-8
; Sequence 8, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; CURRENT FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; EARLIER FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-438-046-8

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Query Match 100.0%; Score 1742; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.8e-172;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LYRDETIQVKGNGYVQSPFPNSYPNLLTTLWRLHSEQNTRIQLVFDNQFGLBEAENDI 60
Db LYRDETIQVKGNGYVQSPFPNSYPNLLTTLWRLHSEQNTRIQLVFDNQFGLBEAENDI 108

Qy 61 CRYDFVEVEDISSTTIIRGWCCHKEVPPRIKSTNQIKITFKSDDYFVAKPGFKIYYS 120
Db CRYDFVEVEDISSTTIIRGWCCHKEVPPRIKSTNQIKITFKSDDYFVAKPGFKIYYS 168

Qy 121 LLEDFOAAAASETWESVTSSISGVSYNSPSTPTLIADALDKKIAEFTVDDLKYFN 180
Db LLEDFOAAAASETWESVTSSISGVSYNSPSTPTLIADALDKKIAEFTVDDLKYFN 228

Qy 181 PESQEDLENNYLDTPRYGRSYHDKRSKVDLDRNLDDAKRYSCTPRNSVNIREEKLA 240
Db PESQEDLENNYLDTPRYGRSYHDKRSKVDLDRNLDDAKRYSCTPRNSVNIREEKLA 288

Qy 241 NVVFFPRCLLVQRCGNGCGCTVNWRSCTCNSGKTVKXYHEVLQFEPGCHKRRGRAKTM 300
Db NVVFFPRCLLVQRCGNGCGCTVNWRSCTCNSGKTVKXYHEVLQFEPGCHKRRGRAKTM 348

Qy 301 LVDIQLDHERCDCICSSRPPR 322
Db LVDIQLDHERCDCICSSRPPR 370

RESULT 10
US-09-540-224-4
; Sequence 4, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-540-224-4

Query Match 89.6%; Score 1561; DB 4; Length 370;
Best Local Similarity 86.6%; Pred. No. 1.2e-153;
Matches 279; Conservative 23; Mismatches 20; Indels 0; Gaps 0;

Qy 1 LYRDETIQVKGNGYVQSPFPNSYPNLLTTLWRLHSEQNTRIQLVFDNQFGLBEAENDI 60
Db LYQREENIQTNSGHVQSPFPNSYPNLLTTLWRLHSEQNTRIQLVFDNQFGLBEAENDI 108

Qy 61 CRYDFVEVEDISSTTIIRGWCCHKEVPPRIKSTNQIKITFKSDDYFVAKPGFKIYYS 120
Db CRYDFVEVEDISSTTIIRGWCCHKEVPPRIKSTNQIKITFKSDDYFVAKPGFKIYYS 168

Qy 109 CRYDFVEVEVESSTTVVRGWCCHKEIPRITSTNQIKITFKSDDYFVAKPGFKIYYS 168
Db CRYDFVEVEVESSTTVVRGWCCHKEIPRITSTNQIKITFKSDDYFVAKPGFKIYYS 228

Qy 121 LLEDFOAAAASETWESVTSSISGVSYNSPSTPTLIADALDKKIAEFTVDDLKYFN 180
Db FVEDFOAAAASETWESVTSSISGVSYNSPSTPTLIADALDKKIAEFTVDDLKYFN 228

Qy 181 PESQEDLENNYLDTPRYGRSYHDKRSKVDLDRNLDDAKRYSCTPRNSVNIREEKLA 240
Db PVSQWDDLENNYLDTPRYGRSYHDKRSKVDLDRNLDDAKRYSCTPRNSVNIREEKLA 288

Qy 241 NVVFFPRCLLVQRCGNGCGCTVNWRSCTCNSGKTVKXYHEVLQFEPGCHKRRGRAKTM 300
Db NVVFFPRCLLVQRCGNGCGCTVNWRSCTCNSGKTVKXYHEVLQFEPGCHKRRGRAKTM 348

RESULT 11
US-09-564-595D-53
; Sequence 53, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa E.
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-564-595D-53

Query Match 89.6%; Score 1561; DB 4; Length 370;
Best Local Similarity 86.6%; Pred. No. 1.2e-153;
Matches 279; Conservative 23; Mismatches 20; Indels 0; Gaps 0;

Qy 1 LYRDETIQVKGNGYVQSPFPNSYPNLLTTLWRLHSEQNTRIQLVFDNQFGLBEAENDI 60
Db LYQREENIQTNSGHVQSPFPNSYPNLLTTLWRLHSEQNTRIQLVFDNQFGLBEAENDI 108

Qy 61 CRYDFVEVEDISSTTIIRGWCCHKEVPPRIKSTNQIKITFKSDDYFVAKPGFKIYYS 120
Db CRYDFVEVEDISSTTIIRGWCCHKEVPPRIKSTNQIKITFKSDDYFVAKPGFKIYYS 168

Qy 109 CRYDFVEVEVESSTTVVRGWCCHKEIPRITSTNQIKITFKSDDYFVAKPGFKIYYS 168
Db CRYDFVEVEVESSTTVVRGWCCHKEIPRITSTNQIKITFKSDDYFVAKPGFKIYYS 228

Qy 121 LLEDFOAAAASETWESVTSSISGVSYNSPSTPTLIADALDKKIAEFTVDDLKYFN 180
Db FVEDFOAAAASETWESVTSSISGVSYNSPSTPTLIADALDKKIAEFTVDDLKYFN 228

Qy 181 PESQEDLENNYLDTPRYGRSYHDKRSKVDLDRNLDDAKRYSCTPRNSVNIREEKLA 240
Db PVSQWDDLENNYLDTPRYGRSYHDKRSKVDLDRNLDDAKRYSCTPRNSVNIREEKLA 288

Qy 241 NVVFFPRCLLVQRCGNGCGCTVNWRSCTCNSGKTVKXYHEVLQFEPGCHKRRGRAKTM 300
Db NVVFFPRCLLVQRCGNGCGCTVNWRSCTCNSGKTVKXYHEVLQFEPGCHKRRGRAKTM 348

RESULT 12
US-09-808-972-4
; Sequence 4, Application US/09808972
; Patent No. 6630142
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROBLASTIC
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 00-79

```
/ CURRENT APPLICATION NUMBER: US/09/808,972
/ CURRENT FILING DATE: 2001-03-14
/ PRIOR APPLICATION NUMBER: US 60/235,295
/ PRIOR FILING DATE: 2000-09-26
/ PRIOR APPLICATION NUMBER: US 09/564,595
/ PRIOR FILING DATE: 2000-05-03
/ PRIOR APPLICATION NUMBER: US 60/180,169
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: US 60/164,463
/ PRIOR FILING DATE: 1999-11-10
/ PRIOR APPLICATION NUMBER: US 60/132,250
/ PRIOR FILING DATE: 1999-05-03
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: FastSeq for Windows Version 3.0.
/ SEQ ID NO 4
/ LENGTH: 370
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-09-808-972-4

Query Match      89.6%; Score 1561; DB 4; Length 370;
Best Local Similarity 86.6%; Pred. No. 1.2e-153;
Matches 279; Conservative 23; Mismatches 20; Indels 0; Gaps 0;

QY 1 LYRDETIQVKGNGVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLGEAEANDI 60
DB 49 LYORENIQVTSNGHVQSPRPNSYPNLLLTWRLHSQENTRIQLSFDHQFGLGEAEANDI 108
QY 61 CRYDFVEVEDISSETTIIRGRWCHEVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYS 120
DB 109 CRYDFVEVEVESSTTVRGRWCHEVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYS 168
QY 121 LLEDFOPAASATNNESVTSSISGVSYNSPSVTPDPTLADALDKKIAEFDTVEDLLKYFN 180
DB 169 FVEDFOPAASATNNESVTSSISGVSYNSPSVTPDPTLADALDKKIAEFDTVEDLLKYFN 228
QY 181 PESWQEDLENMYLDTPRYGRSYHDKRSKVDLRLNDLDAKRYSCPTPNYSVNIREEKLANV 240
DB 229 PVSQWQDLENLYLDTPRYGRSYHDKRSKVDLRLNDLDAKRYSCPTPNYSVNIREEKLANV 288
QY 241 NVVFFPRCLLVORCGNGCGTNNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGAKTMALV 300
DB 289 NAVFFPRCLLVORCGNGCGTNNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGAKTMALV 348
QY 301 LVDIQDLHHERCDCICSSRPPR 322
DB 349 LVDIQDLHHERCDCICSSRPPR 370

RESULT 13
US-09-564-595D-56
/ Sequence 56, Application US/09564595D
/ Patent No. 6495668
/ GENERAL INFORMATION:
/ APPLICANT: Gilbert, Teresa
/ APPLICANT: Hart, Charles E.
/ APPLICANT: Sheppard, Paul O.
/ TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
/ FILE REFERENCE: 99-19
/ CURRENT APPLICATION NUMBER: US/09/564,595D
/ CURRENT FILING DATE: 2000-05-03
/ PRIOR APPLICATION NUMBER: US 09/304,216
/ PRIOR FILING DATE: 1999-05-03
/ PRIOR APPLICATION NUMBER: US 60/164,463
/ PRIOR FILING DATE: 1999-11-10
/ PRIOR APPLICATION NUMBER: US 60/180,169
/ PRIOR FILING DATE: 2000-02-04
/ NUMBER OF SEQ ID NOS: 57
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 56
/ LENGTH: 317
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: fusion polypeptide
US-09-564-595D-55

Query Match      77.9%; Score 1357.5; DB 4; Length 316;
Best Local Similarity 80.0%; Pred. No. 1.3e-132;
Matches 256; Conservative 24; Mismatches 33; Indels 7; Gaps 4;

QY 5 DETIQVKGNGVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLGEAEANDICRY 63
DB 2 ERITVTSTNGSIHSPRPHTYPRNTLVLRVAVENWVLIQTLTDFDEGLDEPDIDICKY 61
QY 64 DFVEVEDISSETTIIRGRWCHEVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYS-L 122
DB 62 DFVEVEPSDGT--ILGRWCSTGTPGKQISGKQIRIRFVSDVDFPSPERFCIHNVIM 119
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/ FEATURE:
/ OTHER INFORMATION: fusion polypeptide
US-09-564-595D-56

Query Match      80.5%; Score 1403; DB 4; Length 317;
Best Local Similarity 83.8%; Pred. No. 2.5e-137;
Matches 263; Conservative 14; Mismatches 33; Indels 4; Gaps 2;

QY 4 RDETIQVKGNGVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLGEAEANDICRY 63
DB 1 RDETIQVKGNGVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLGEAEANDICRY 60
QY 64 DFVEVEDISSETTIIRGRWCHEVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYS-L 123
DB 61 DFVEVEDISSETTIIRGRWCHEVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYS-L 120
QY 124 DFQPAASATNNESVTSSISGVSYNSPSVTPDPTLADALDKKIAEFDTVEDLLKYFN 183
DB 121 DFQPAASATNNESVTSSISGVSYNSPSVTPDPTLADALDKKIAEFDTVEDLLKYFN 180
QY 184 WOEDLENNMYLDTPRYGRSYHDKRSK-VLDLRLNDLDAKRYSCPTPNYSVNIREEKLANV 242
DB 191 WOEDLENNMYLDTPRYGRSYHDKRSKVDLRLNDLDAKRYSCPTPNYSVNIREEKLANV 240
QY 243 VFFPRCLLVORCGNGCGTNNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGAKTMALV 302
DB 241 IFWPGLLVKRCGNGCACCLHNCNECQVPSKVTKKYHEVLQFEPGHIKRRGAKTMALV 302
QY 303 DIQDLHHERCDCIC 316
DB 298 DVALEHHEECDCVC 311

RESULT 14
US-09-564-595D-55
/ Sequence 55, Application US/09564595D
/ Patent No. 6495668
/ GENERAL INFORMATION:
/ APPLICANT: Gilbert, Teresa
/ APPLICANT: Hart, Charles E.
/ APPLICANT: Sheppard, Paul O.
/ TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
/ FILE REFERENCE: 99-19
/ CURRENT APPLICATION NUMBER: US/09/564,595D
/ CURRENT FILING DATE: 2000-05-03
/ PRIOR APPLICATION NUMBER: US 09/304,216
/ PRIOR FILING DATE: 1999-05-03
/ PRIOR APPLICATION NUMBER: US 60/164,463
/ PRIOR FILING DATE: 1999-11-10
/ PRIOR APPLICATION NUMBER: US 60/180,169
/ PRIOR FILING DATE: 2000-02-04
/ NUMBER OF SEQ ID NOS: 57
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 55
/ LENGTH: 316
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: fusion polypeptide
US-09-564-595D-55

Query Match      77.9%; Score 1357.5; DB 4; Length 316;
Best Local Similarity 80.0%; Pred. No. 1.3e-132;
Matches 256; Conservative 24; Mismatches 33; Indels 7; Gaps 4;

QY 5 DETIQVKGNGVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLGEAEANDICRY 63
DB 2 ERITVTSTNGSIHSPRPHTYPRNTLVLRVAVENWVLIQTLTDFDEGLDEPDIDICKY 61
QY 64 DFVEVEDISSETTIIRGRWCHEVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYS-L 122
DB 62 DFVEVEPSDGT--ILGRWCSTGTPGKQISGKQIRIRFVSDVDFPSPERFCIHNVIM 119
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Search completed: October 29, 2004, 23:33:57
Job time : 40 secs

Qy 123 EDFQPAASATNWSVTSSISGVSNPSVTDPTLIADALDKIAEFTVDELLKYFNPE 182
Db 120 PQFTEA---ETNWSVTSSISGVSNPSVTDPTLIADALDKIAEFTVDELLKYFNPE 176
Qy 183 SQWEDLENNYLDTPRYGRSYHDKRSKVDLRLNDLNDADAKRYCTPRNYSVNIREEKLKLV 242
Db 177 SQWEDLENNYLDTPRYGRSYHDKRSKVDLRLNDLNDADAKRYCTPRNYSVNIREEKLKLV 236
Qy 243 VFFPRCLLVQRCGCGGCTVNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRKTMALV 302
Db 237 VFFPRCLLVQRCGCGGCTVNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRKTMALV 296
Qy 303 DIQLDHERCDCICSSRPPR 322
Db 297 DIQLDHERCDCICSSRPPR 316

RESULT 15

US-09-564-595D-57
; Sequence 57, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-57

Query Match 62.9%; Score 1095; DB 4; Length 303;
Best Local Similarity 67.4%; Pred. No. 2.5e-105;
Matches 213; Conservative 26; Mismatches 55; Indels 22; Gaps 5;
Qy 4 RDETIQVKGNGYVQSPRPFPNSYPNRLLTWRLHSQENTRIQLVFDNQFGLBEAENDICRY 63
Db 1 RDETIQVKGNGYVQSPRPFPNSYPNRLLTWRLHSQENTRIQLVFDNQFGLBEAENDICRY 60
Qy 64 DFVEVEDISETTIIRGWCCHKEVPPRIKSRNQIKITFKSDDYFVAKPGFKIYYSLL 123
Db 61 DFVEVEDISETTIIRGWCCHKEVPPRIKSRNQIKITFKSDDYFVAKPGFKIYYSLL 120
Qy 124 DFQPAASATNWSVTSSISGVSNPSVTDPT-LIADALDKIAEFTVDELLKYFNPE 182
Db 121 DFQPAASV-----SPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPE 164
Qy 183 SQWEDLENNYLDTPRYGRSY-HDKRSK-VDLRLNDLNDADAKRYCTPRNYSVNIREEKLK 240
Db 165 RWQLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLITEEVRLYSCYCTPRNFSVIREELKRT 224
Qy 241 NVVFPFRCCLLVORCGCGGCTVNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRKTM 300
Db 225 DTIFWPGCLLVKRCGCGNACCLHNCNECCQVPSKVKYHEVLQLRP---KTGVRGLHKS 281
Qy 301 LVDIQLDHERCDCIC 316
Db 282 LTDVALEHHECDCVC 297

	Matches	54;	Conservative	36;	Mismatches	72;	Indels	45;	Gaps	10;
Qy	10	VKNGYVOSPRFPNSYPNNLLLTWRLHSQENTRIQLVPDNOQGLGEEAENDICRYDFVEVE	69	:	:	:	:	:	:	:
Dz	435	LKKKGMIYSNPYPDYPRLTKCSMIIIEAPENHIVKLAKFD-FNVEYGHG--CIYDAVEVY	491	:	:	:	:	:	:	:
Qy	70	DISETSTIIRRCWCHEKEVPPIKRSTRNQIKITFKSP---DYFVAKPGEFI-	117	:	:	:	:	:	:	:
Dz	492	DGAEEKOLI-ARLCGY-TLPLUPISPPNTMLIREFTDMENS----	PGRVKVFSEVPPEK	545	:	:	:	:	:	:
Qy	118	YVSILLEDFAAASSETNWESSTISSIGSVSNPSVDPTTLTADALDKKIAEFTVEDLLK	177	:	:	:	:	:	:	:
Dz	546	QFSLPVDDTP-TISMLHPRAILDVCGWAMPPTKWLLPRIVG-----E	588	:	:	:	:	:	:	:
Qy	178	YNPSESQEEDLENNMYLDTPVRGRSYH	204	:	:	:	:	:	:	:
Dz	589	EASPNSWPQVOIQIFL-----RTFH	608	:	:	:	:	:	:	:

RESULT 14
S58984
development protein tolkin (EC 3.4.24.-) - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: S58984
R:Finelli, A.L.; Xie, T.; Bossie, C.A.; Blackman, R.K.; Padgett, R.W.
Genetics 141, 271-281, 1995
A:Title: The tolkin gene is a tolloid/BMP-1 homologue that is essential for *Drosophila* d
A:Reference number: S58984; MUID:96042912; PMID:8536976
A:Accession: S58984
A:Molecule type: mRNA
A:Residues: 1-1464 <FIN>
A:Cross-references: UNIPROT:Q24132; EMBL:U34777; NID:gl002985; PIDN:AAC47015.1; PID:gl00
A:Note: the authors did not translate the codon for residue 722
C:Genetics:
A:Gene: tolkin
A:Cross-references: FlyBase:FBgn0004885
C:Keywords: hydrolase; metalloproteinase; zinc
F:529-722/Domain: atascain homology <ASI>
F:958-993/Domain: EGF homology <EGF>
F:1118-1153/Domain: EGF homology <EGF1>
F:614,618,624,673/Binding site: zinc (His, His, His, Tyr) #status predicted
F:615/Active site: Glu #status predicted

		8.7%;	Score	151.5;	DB	2;	Length	1464;
		Best Local Similarity		36.4%;		Pred.		No. 0.0019;
		Matches		39;		Conservative		18;
						Mismatched		45;
						Indels		5;
						Gaps		4;
Qy	14	GYYVSPRPNSYPNLLLTWRILHSQEINTRQLVFDPNQFGLSEAENDICRYDFVEVDISE	73	:	:	:	:	:
Dd	1167	GTIFSNPYDPSYPPNADCVWHFITTPGHRIKLIF-NEFDVESHQE--CTYDNVAAYDGES	1223	:	:	:	:	:
Qy	74	TSTIIRGCWCHKEVPPIKSRITNOIKITPKSDDYFYVAKGFKIYS	120	:	:	:	:	:
Dd	1224	ESSVLGRFCGDK-IPPFISSTSNQMYMLVKTDKN-KQQKGFTASHS	1368	:	:	:	:	:

RESULT 15
T31069
tolloid-BMP-1 like protein 1 - California sea hare
N;Alternate names: probable metalloprotease TBL-1
C;Species: Aplysia californica (California sea hare)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31069
R;Liu, Q.R.; Hattar, S.; Endo, S.; MacPhee, K.; Zhang, H.; Cleary, L.J.; Byrne, J.H.; Es
J. Neurosci. 17, 755-764, 1997
A;Title: A developmental gene (Tolloid/BMP-1) is regulated in Aplysia Neurons by treatme
A;Reference number: Z20965; MUID:98007484; PMID:8987797
A;Accession: T31069
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1070 <LIU>
A;Cross-references: UNIPROT:P91972; EMBL:U57369; NID:g1899041; PID:g1899042; PIDN:AAC474

DB	1049	LYDYTDNFGMLSPNFPNNYPSNWECIYRITVGLNQIALHFTDTL-EDYFGSQCVDFV	1107
QY	171	TVED	174
DB	1108	EIRD	1111

RESULT 12

QJ0948

A5 Antigen precursor - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000

C:Accession: JH0466; JQ0948

R:Takagi, S.; Hirata, T.; Agata, K.; Mochii, M.; Eguchi, G.; Fujisawa, H.

Neuron 7, 295-307, 1991

A:Title: The A5 antigen, a candidate for the neuronal recognition molecule, has homologies with the A5 antigen precursor of the African clawed frog

A:Reference number: JH0466; MUID:91337458; PMID:1908252

A:Accession: JH0466

A:Molecule type: mRNA

A:Residues: 1-927 <TAK>

A:Cross-references: GB:D01077; NID:G222962; PIDN:BR001260.1; PID:G222963

A:Experimental source: Tadpole, brain

A:Note: This protein has motifs homologous to complement components C1r and C1s and to co-receptors for the neuronal recognition molecule involved in the neuronal recognition

C:Comment: This protein is a neuronal cell surface molecule; discoidein I amino-terminal homology

C:Superfamily: Xenopus A5 antigen; C1r/C1s repeat homology; transmembrane protein

C:Keywords: duplication; glycoprotein; transmembrane protein

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-927/Product: A5 antigen #status predicted <A5A>

F:27-136/Domain: C1r/C1s repeat homology <C1r1>

F:147-262/Domain: C1r/C1s repeat homology <C1r2>

F:274-424/Domain: discoidein I amino-terminal homology <DN1>

F:430-584/Domain: discoidein I amino-terminal homology <DN2>

F:646-812/Domain: MAM homology <MAM>

F:861-883/Domain: transmembrane #status predicted <TM>

F:150,261,300,523,844/Binding site: carbohydate (Asn) (covalent) #status predicted

Query Match	9.8%	Score 171.5;	DB 1;	Length 927;
Best Local Similarity	30.6%	Pred. No. 3e-05;		
Matches	53;	Conservative	29;	Mismatches 78; Indels 13; Gaps 7;

QY 6 ETIQKNGYVQSPFPNSYPRNLLTWLHSGEN-TRIQLVPDNOFGLAEANDICRYD 64

DB 29 DTIKTSPSYLTSAGYPHSPPSQRCWEIQAPEYQRIQMINFNPHFDLSRE---CKYD 85

QY 65 FVEVEDISETSIIIGRWGCHKEVPRIKSRNQIKITFKSDYFVAKPGFKIYYSLLED 124

DB 86 YVEVIEDGNANQLGLKYGCG-KIAPSPVSTGPSIFIRFVS-DYETPGAGFSIRY---EV 140

QY 125 FOPAAASSETNWSVTSISGSVY--NSPSVTDPTLI--ADALDKKIAEFTVE 173

DB 141 FTGTGECSENFTSSNGVIKSPKYPEKYPNALECTYIIFAPKMQBIVLEFESFE 193

RESULT 13

T30337

polyprotein - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

C:Accession: T30337

R:Yang, J.C.; Lindsay, L.L.; Hedrick, J.L. 1998

A:Description: cDNA cloning of ovochymase, a chymotrypsin-like protease released from Xenopus laevis

A:Reference number: Z20829

A:Accession: T30337

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-1524 <YAN>

A:Cross-references: UNIPROT:Q91674; EMBL:U81290; NID:G2981640; PID:G2981641; PIDN:AAC2474

C:Superfamily: trypsin related polyprotein; trypsin homology

Query Match	9.0%	Score 156.5;	DB 2;	Length 1524;
Best Local Similarity	26.1%	Pred. No. 0.00084;		

C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; gl
F:1-22/Domain: signal sequence C-status predicted <SIG>
F:23-986/Product: procollagen C-endopeptidase tolloid-like splice form #status predicted
F:130-321/Domain: astacin homology <AST>
F:322-431/Domain: C1r/C1s repeat homology <C1R1>
F:435-544/Domain: C1r/C1s repeat homology <C1R2>
F:551-587/Domain: EGF homology <EG1>
F:591-700/Domain: C1r/C1s repeat homology <C1R3>
F:707-742/Domain: EGF homology <EG2>
F:747-856/Domain: C1r/C1s repeat homology <C1R4>
F:860-973/Domain: C1r/C1s repeat homology <C1R5>
F:91-142,332,363,599/Binding site: carbonydrate (Asn) (covalent) #status predicted
F:191,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66
F:213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted
F:214/Active site: Glu #status predicted
F:565,720/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 10.8%; Score 187.5; DB 1; Length 986;
Best Local Similarity 39.4%; Pred. No. 1.9e-06;
Matches 43; Conservative 18; Mismatches 43; Indels 5; Gaps 3;

QY 11 KGVGVQSPFPNSYPNRLLLTWRLHSQENTRIQLVFNQFGLGEAENDICRYDFVEVED 70
DB 597 KLNGSITSPGWKEPPNKNKCIWLVAPQYRISLQFD---FFETEGNDVCKYDFVEVRS 653

QY 71 ISETSTIIRGWCCHKVEPPRIKSRNQIKITFKSDDYFVAKPGKIYY 119
DB 654 GLTADSKLHGKFCG-SEKPEVITSQYNNMRVEFKSDN-TVSKKGFKAHF 700

RESULT 8
149540
C:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; E
C:Keywords: hydrolase; metalloproteinase; zinc
F:135-326/Domain: astacin homology <AST>
F:556-592/Domain: EGF homology <EG1>
F:596-705/Domain: C1r/C1s repeat homology <C1R>
F:712-747/Domain: EGF homology <EG2>
F:218,222,228,277/Binding site: zinc (His, His, His, Tyr) #status predicted
F:219/Active site: Glu #status predicted

Query Match 10.8%; Score 187.5; DB 2; Length 991;
Best Local Similarity 39.4%; Pred. No. 1.9e-06;
Matches 43; Conservative 18; Mismatches 43; Indels 5; Gaps 3;

QY 11 KGVGVQSPFPNSYPNRLLLTWRLHSQENTRIQLVFNQFGLGEAENDICRYDFVEVED 70
DB 602 KLNGSITSPGWKEPPNKNKCIWLVAPQYRISLQFD---FFETEGNDVCKYDFVEVRS 658

QY 71 ISETSTIIRGWCCHKVEPPRIKSRNQIKITFKSDDYFVAKPGKIYY 119
DB 659 GLTADSKLHGKFCG-SEKPEVITSQYNNMRVEFKSDN-TVSKKGFKAHF 705

RESULT 9
T09456
C:Superfamily: drosophila dorsal-ventral patterning protein tolloid; astacin homology; C1r/C1s repeat
C:Keywords: duplication; hydrolase; metalloproteinase; zinc
F:136-329/Domain: astacin homology <AST>
F:352-464/Domain: C1r/C1s repeat homology <C1R1>
F:468-578/Domain: C1r/C1s repeat homology <C1R2>
F:585-620/Domain: EGF homology <EG1>

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T09456
R:Kozvaki, R.; Kristiansen, M.; Silahcaroglu, A.; Hansen, C.; Tommerup, N.
Blood 91. 3593-3600. 1998
A:Title: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular characteriz
ion.
A:Reference number: Z16677; MUID:98241400; PMID:9572993
A:Accession: T09456
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-3623 <KOZ>
A:Cross-references: UNIPROT:O60494; EMBL:AF034611; NID:g3929528; PIDN:AA082612.1; PID:g3
C:Genetics:
A:Map position: 10p12
C:Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology
C:Keywords: receptor; vitamin B12 uptake
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-3623/Product: intrinsic factor-B12 receptor #status predicted <MAT>
F:436-467/Domain: EGF homology <EGF>

Query Match 10.6%; Score 184.5; DB 2; Length 3623;
Best Local Similarity 24.3%; Pred. No. 1.7e-05;
Matches 85; Conservative 34; Mismatches 120; Indels 11; Gaps 17;

QY 8 IQVKGNGVQSPFPNSYPNRLLLTWRLHSQENTRIQLVFNQFGLGEAENDICRYDFVE 67
DB 935 ILTESTGTIQSPGHNVYPHGINCTWHILVQPNHLHLMFET-PHLEPHYN--CTNDYLE 991

QY 68 VEDI-SETSTIIRGWCCHKVEPPRIKSRNQIKITFKSDDYFVAKPGKIYY----- 119
DB 992 VYDTSSETSL---GRYCG-KSIPPSLTSSGSLMLVFTYDS-DLAYEGFLINYEISAAT 1046

QY 120 SLLEDFQPAASET-----NWESVTSSISGVSNPSVPTDPTLIADALDKIAEF 169
DB 1047 ACLQDYTDLLGTFSTPFPNPNWECI-----YRI-TVRTGQLIA----- 1087

QY 170 DTVEDLLKYNPESQEDLENMILDTPIYGRSY-----HDKR-- 207
DB 1088 -----VHFTNFSLEAIGNVYTDLEIRDGGYEKSPLLGIFYGSLNPPTIISHNKLW 1140

QY 208 SKVDLDRLLDAKYSCTPRNYSVNIRELKLANVVFPRCLLVORCGNCCGCTVNWRS 267
DB 1141 LKFKSDQI-DTRSGFSAYWDGSGTG-----COGN----- 1168

QY 268 CTCNSGKTVKVKYHVELOPEPGHI-----KRRGRKTAKTALVDIQLDHHRC 312
DB 1169 LTTSSGTFISPNYPMPYHSSECYWKLKSSHGSFAFEKDFHLEHPNC 1218

RESULT 10
A39288
C:Superfamily: drosophila dorsal-ventral patterning protein tolloid (EC 3.4.24.-) - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A39288
R:Shimell, M.J.; Ferguson, E.L.; Childs, S.R.; O'Connor, M.B.
Cell 67. 469-481. 1991
A:Title: The Drosophila dorsal-ventral patterning gene tolloid is related to human bone
C:Reference number: A39288; MUID:92034970; PMID:1840509
A:Accession: A39288
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1057 <SHI>
A:Cross-references: UNIPROT:P25723; GB:M76976; NID:g157305; PIDN:AAA28491.1; PID:g157306
C:Genetics:
A:Gene: FlyBase:tlld
A:Cross-references: FlyBase:FBgn0003719
C:Superfamily: dorsal-ventral patterning protein tolloid; astacin homology; C1r/C1s repeat
C:Keywords: duplication; hydrolase; metalloproteinase; zinc
F:136-329/Domain: astacin homology <AST>
F:352-464/Domain: C1r/C1s repeat homology <C1R1>
F:468-578/Domain: C1r/C1s repeat homology <C1R2>
F:585-620/Domain: EGF homology <EG1>

```
Matches 71; Conservative 33; Mismatches 89; Indels 54; Gaps 11;
Qy 11 KNGGVQSPRPNSYPNLLTLRLHSGENTRIOLVFNQFGLAEANDICRYDFVEVED 70
Db 597 KNGSITSPGWPKYPPNKNCIWQVAPQVRIQLQFD---FFTEGNDVCKYDFVEVRS 653
Qy 71 ISETSTIIRGWCQHGKEVPPRIKSRNQIKITFKSDDYFVAKPGFKI--YYSLLE-----123
Db 654 GLTADSKLHGKFCG-SEKPEVITSQYNNMRVEFKSDN-TVSKKGFKAHFVSLEAGDRH 711
Qy 124 -----DFQPAASSTWESVTSISGVSNPSVTD-----PTLIADALD 163
Db 712 SHLSGLELLCPHALVDTPAPPALSGDTHAHTHTVHTHCPIAQETCRGPPLGASRLS 771
Qy 164 KKIAEFDFVEDLLKYFNESQEDLENWYLD-TPRYGRSVHDKRSKVDLRLNDDAKRY 222
Db 772 PQGCHLTLA-----EQ-----EGSYLDFWDTHRG-----DPKPR-----RRRSLKTF 810
Qy 223 SCTPRNY 229
Db 811 SLTPATF 817
RESULT 5
JC2218
procollagen C-endopeptidase (EC 3.4.24.19) - African clawed frog (clone 22AN)
N:Alternate names: bone morphogenic protein 1
C:Species: Xenopus laevis (African clawed frog)
C>Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
C:Accession: JC2218
R:Maeno, M.; Xue, Y.; Wood, T.I.; Ong, R.C.; Kung, H.
Gene 134, 257-261, 1993
A:Title: Cloning and expression of cDNA encoding Xenopus laevis bone morphogenetic prote
A:Reference number: JC2218; MUID:94085787; PMID:8262384
A:Accession: JC2218
A:Molecule type: mRNA
A:Residues: 1-707 <MA5>
A:Cross-references: UNIPROT:P98070; GB:L12249; NID:G406540; PIDN:AAA16313.1; PID:G406541
C:Comment: This protein induces ectopic cartilage formation in vivo.
C:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; E
C:Keywords: beta-hydroxyasparagine, glycoprotein, hydrolase, metalloproteinase, zinc
F:193-284/Domain: astacin homology <AST>
F:285-397/Region: complement 1r/1s-like repeat
F:285-397/Region: complement 1r/1s-like repeat
F:398-510/Region: complement 1r/1s-like repeat
F:398-510/Region: complement 1r/1s-like repeat
F:514-550/Domain: EGF homology <EGF>
F:554-666/Region: complement 1r/1s-like repeat
F:554-663/Domain: C1r/C1s repeat homology <C1R3>
F:621,105,295,326/Binding site: carboxylate (Asn) (covalent) #status predicted
F:176,180,186,235/Binding site: zinc (His, His, His, His, Tyr) #status predicted
F:177/Active site: Glu #status predicted
F:528/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
Query Match 10.9%; Score 189.5; DB 2; Length 707;
Best Local Similarity 42.5%; Pred. No. 8.5e-07;
Matches 45; Conservative 18; Mismatches 38; Indels 5; Gaps 4;
Qy 11 KNGGVQSPRPNSYPNLLTLRLHSGENTRIOLVFNQFGLAEANDICRYDFVEVED 70
Db 560 KNGSINSPGWPKYPPNKNCIWQVAPQVRIQLQFD-QF--FTEGNDVCKYDFVEVRS 616
Qy 71 ISETSTIIRGWCQHGKEVPPRIKSRNQIKITFKSDDYFVAKPGFK 116
Db 617 GLTSDSKLHGKFCG-SELPVITTSQYNNMRVEFKSDN-TVSKKGFKQ 660
RESULT 6
BMHUI
procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form BMP1 - human
N:Alternate names: bone morphogenic protein 1 (BMP1)
C:Species: Homo sapiens (man)
C>Date: 16-Sep-1992 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
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C:Accession: A37278; E58788
R:Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; Hewi
Science 242, 1528-1534, 1998
A:Title: Novel regulators of bone formation: molecular clones and activities.
A:Reference number: A37278; MUID:89072730; PMID:3201241
A:Accession: A37278
A:Molecule type: mRNA
A:Residues: 1-730 <WOZ>
A:Cross-references: GB:M22488; NID:G179499; PIDN:AAA51833.1; PID:G179500
C:Genetics:
A:Gene: GDB:BMP1
A:Cross-references: GDB:125203; OMIM:112264
A:Map position: 8p21-8p21
C:Function:
A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type
C:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; E
C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; gl
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-730/Product: procollagen C-endopeptidase splice form BMP1 #status predicted <MAT>
F:130-321/Domain: astacin homology <AST>
F:322-431/Domain: C1r/C1s repeat homology <C1R1>
F:435-544/Domain: C1r/C1s repeat homology <C1R2>
F:551-587/Domain: EGF homology <EGF>
F:591-700/Domain: C1r/C1s repeat homology <C1R3>
F:91,142,332,363,599/Binding site: carboxylate (Asn) (covalent) #status predicted
F:163-319,185-205,322-348,375-397,435-461,489-510,551-553,559-572,574-587,591-617,644-66
F:213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted
F:214/Active site: Glu #status predicted
F:565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
Query Match 10.8%; Score 187.5; DB 1; Length 730;
Best Local Similarity 39.4%; Pred. No. 1.3e-06;
Matches 43; Conservative 18; Mismatches 43; Indels 5; Gaps 3;
Qy 11 KNGGVQSPRPNSYPNLLTLRLHSGENTRIOLVFNQFGLAEANDICRYDFVEVED 70
Db 597 KNGSITSPGWPKYPPNKNCIWQVAPQVRIQLQFD---FFTEGNDVCKYDFVEVRS 653
Qy 71 ISETSTIIRGWCQHGKEVPPRIKSRNQIKITFKSDDYFVAKPGFKIYY 119
Db 654 GLTADSKLHGKFCG-SEKPEVITSQYNNMRVEFKSDN-TVSKKGFKAHF 700
RESULT 7
B58788
procollagen C-endopeptidase (EC 3.4.24.19) precursor, tollid-like splice form - human
N:Alternate names: bone morphogenic protein 1, tollid-like splice form
C:Species: Homo sapiens (man)
C>Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 09-Jul-2004
C:Accession: A37278; B58788
R:Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; Hewi
Science 242, 1528-1534, 1998
A:Title: Novel regulators of bone formation: molecular clones and activities.
A:Reference number: A37278; MUID:89072730; PMID:3201241
A:Accession: A37278
A:Molecule type: mRNA
A:Residues: 1-702, 'EKRPALQPPRPHQLKFRVQKRNRPQ' <WOZ>
A:Cross-references: UNIPROT:P13497; GB:M22488; NID:G179499; PIDN:AAA51833.1; PID:G179500
R:Takahara, K.; Lyons, G.E.; Greenspan, D.S.
J. Biol. Chem. 269, 32572-32578, 1994
A:Title: Bone morphogenetic protein-1 and a mammalian tollid homologue (mTld) are encode
A:Reference number: A58788; MUID:95096114; PMID:7798260
A:Accession: B58788
A:Molecule type: mRNA
A:Residues: 703-986 <TAK>
A:Cross-references: GB:L35279; NID:G619860; PIDN:AAC41710.1; PID:G619861
C:Genetics:
A:Gene: GDB:BMP1; BMP-1
A:Cross-references: GDB:125203; OMIM:112264
A:Map position: 8p21-8p21
C:Function:
A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type
C:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; E
```

JC7592
spinal cord-derived growth factor-B precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C:Accession: JC7592
R:Hamada, T.; Uti-Tai, K.; Imaki, J.; Miyata, Y.
Biochem. Biophys. Res. Commun. 280, 733-737, 2001
A:Title: Molecular cloning of SCDGF-B, a novel growth factor homologous to SCDGF/PDGF-C/
F:152-170/Region: CUB domain #status predicted
A:Reference number: JC7591; MUID:21092670; PMID:11162582
A:Contents: Fetal brain
A:Accession: JC7592
A:Molecule type: mRNA
A:Residues: 1-370 <HAM>
A:Cross-references: UNIPROT:Q9EQT1; DBJ:AB052170
C:Genetics:
F:1-17/Domain: secretory signal sequence #status predicted <SIG>
F:18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>
F:52-170/Region: CUB domain #status predicted
F:272-370/Region: homologous to platelet-derived growth factor/vascular endothelial growth
F:294-308/Region: conserved motif #status predicted

Query Match 90.0%; Score 1567; DB 2; Length 370;
Best Local Similarity 87.0%; Pred. No. 2.6e-114; Mismatches 20; Indels 0; Gaps 0;
Matches 280; Conservative 22; Mismatches 20; Indels 0; Gaps 0;

QY 1 LYRRDETIQKNGYVQSPFPNSYPNLLLTWRLHSEQENTRIQLVFNQFGLGEAEANDI 60
DB 49 LYRRDENIRVTGTHVQSPFPNSYPNLLLTWRLHSEQENTRIQLAFDHFQGLGEAEANDI 108
QY 61 CRYDFVEVEDISSTIIRGWCHEVPPRIKSTNQIKITFKSDDDYFVAKPGFKIYYS 120
DB 109 CRYDFVEVEDISSTIIRGWCHEVPPRIKSTNQIKITFKSDDDYFVAKPGFKIYYS 168
QY 121 LLEDFOPAASATNWSVTSISGVSYNSPSVTDPTLIADALDKKIAEFTDVEDLLKYFN 180
DB 169 FVEDFOPEAASETNWSVTSISGVSYNSPSVTDPTLIADALDKKIAEFTDVEDLLKYFN 228
QY 181 PESWQEDLENMYLDPYRGSRHYDRKSKVDLRLNDLDAKRYSCPTPNYSVNVIREELKLA 240
DB 229 PASWQDDLENLYDTPYRGSRHYDRKSKVDLRLNDLDAKRYSCPTPNYSVNVIREELKLT 288
QY 241 NVVFPFRCLLVQRCGNCGGCTVNNRSCTNCGTKVKKYHEVLQPEPGHKKRGRGAKTMA 300
DB 289 NAVFPFRCLLVQRCGNCGGCTVNNRSCTNCGTKVKKYHEVLQPEPGHKKRGRGAKTMA 348
QY 301 LVDIQLDHHERCDCICSSRPPR 322
DB 349 LVDIQLDHHERCDCICSSRPPR 370

RESULT 3
JC7998
platelet-derived growth factor-D - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Nov-2003 #sequence_revision 10-Nov-2003 #text_change 24-Nov-2003
C:Accession: JC7998
R:Zhao, Y.; Hoyle, G.W.; Zhang, J.; Morris, G.; Lasky, J.A.
Biochem. Biophys. Res. Commun. 308, 126-132, 2003
A:Title: A novel murine PDGF-D splicing variant results in significant differences in pe
A:Reference number: JC7998; PMID:12890490
A:Accession: JC7998
A:Molecule type: mRNA
A:Residues: 1-370 <ZHU>
C:Comment: This protein is a potent mesenchymal cell mitogen and chemoattractant involve
C:Genetics:
A:Gene: pdgf-D
A:Introns: 42/2; 110/1; 170/2; 191/2; 258/2; 330/1; 334/2
C:Keywords: fibrosis; PDGF-D

Query Match 89.6%; Score 1561; DB 2; Length 370;
Best Local Similarity 86.8%; Pred. No. 7.5e-114; Mismatches 23; Indels 0; Gaps 0;
Matches 279; Conservative 23; Mismatches 20; Indels 0; Gaps 0;

QY 1 LYRRDETIQKNGYVQSPFPNSYPNLLLTWRLHSEQENTRIQLVFNQFGLGEAEANDI 60
DB 49 LYQREENIQVTSNGHVQSPFPNSYPNLLLTWRLHSEQENTRIQLSFDHFQGLGEAEANDI 108
QY 61 CRYDFVEVEDISSTIIRGWCHEVPPRIKSTNQIKITFKSDDDYFVAKPGFKIYYS 120
DB 109 CRYDFVEVEDISSTIIRGWCHEVPPRIKSTNQIKITFKSDDDYFVAKPGFKIYYS 168
QY 121 LLEDFOPAASATNWSVTSISGVSYNSPSVTDPTLIADALDKKIAEFTDVEDLLKYFN 180
DB 169 FVEDFOPEAASETNWSVTSISGVSYNSPSVTDPTLIADALDKKIAEFTDVEDLLKYFN 228
QY 181 PESWQEDLENMYLDPYRGSRHYDRKSKVDLRLNDLDAKRYSCPTPNYSVNVIREELKLA 240
DB 229 PVSQDDLENLYDTPYRGSRHYDRKSKVDLRLNDLDAKRYSCPTPNYSVNVIREELKLT 288
QY 241 NVVFPFRCLLVQRCGNCGGCTVNNRSCTNCGTKVKKYHEVLQPEPGHKKRGRGAKTMA 300
DB 289 NAVFPFRCLLVQRCGNCGGCTVNNRSCTNCGTKVKKYHEVLQPEPGHKKRGRGAKTMA 348
QY 301 LVDIQLDHHERCDCICSSRPPR 322
DB 349 LVDIQLDHHERCDCICSSRPPR 370

RESULT 4
A58788
procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form HIS - human
N:Alternate names: bone morphogenic protein splice form BMP-1/HIS
C:Species: Homo sapiens (man)
C:Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 18-Jun-1999
C:Accession: A37278; A58788
R:Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mittleman, B.; Whitters, M.J.; Kriz, R.W.; Hewi
Science 242, 1528-1534, 1988
A:Title: Novel regulators of bone formation: molecular clones and activities.
A:Reference number: A37278; MUID:89072730; PMID:3201241
A:Accession: A37278
A:Molecule type: mRNA
A:Residues: 1-702; 'EKRPALQPPRRPHQKFRVQKNRTPQ' <WOZ>
A:Cross-references: GB:M22488; NID:gl79499; PIDN:AA51833.1; PID:gl79500
R:Takahara, K.; Lyons, G.E.; Greenspan, D.S.
J. Biol. Chem. 269, 32572-32578, 1994
A:Title: Bone morphogenetic protein-1 and a mammalian tollid homologue (mTid) are encode
A:Reference number: A58788; MUID:95096114; PMID:7798260
A:Accession: A58788
A:Molecule type: mRNA
A:Residues: 703-823 <TAK>
A:Cross-references: GB:L35278; NID:9619423; PIDN:AAC41703.1; PID:9619424
C:Genetics:
A:Gene: BMP1; BMP-1
A:Cross-references: GDB:125203; OMIM:112264
A:Map position: 8p21-8p21
C:Function:
A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type
C:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; E
C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; gl
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-823/Product: procollagen C-endopeptidase splice form HIS #status predicted <MAT>
F:130-321/Domain: astacin homology <AST>
F:322-431/Domain: C1r/C1s repeat homology <C1R1>
F:435-544/Domain: C1r/C1s repeat homology <C1R2>
F:551-587/Domain: EGF homology <EGF>
F:591-700/Domain: C1r/C1s repeat homology <C1R3>
F:738-753/Region: histidine-rich
F:9114213232363599/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-661
F:213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted
F:214/Active site: Glu #status predicted
F:565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 11.1%; Score 193; DB 1; Length 823;
Best Local Similarity 28.7%; Pred. No. 5.5e-07;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 29, 2004, 23:24:02 ; Search time 39 Seconds
(without alignments)
794.405 Million cell updates/sec

Title: US-10-086-623-6

Perfect score: 1742

Sequence: 1 LYRDETIQVKGNGYVQSPR.....DIQLDHHERCDCICSSRPPR 322

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1736	99.7	370	2 JC7591	spinal cord-derive
2	1567	90.0	370	2 JC7592	spinal cord-derive
3	1561	89.6	370	2 JC7998	platelet-derived g
4	193	11.1	823	1 AS8788	procollagen C-endo
5	189.5	10.9	707	2 JC2218	procollagen C-endo
6	187.5	10.8	730	1 BMH01	procollagen C-endo
7	187.5	10.8	986	1 B58788	procollagen C-endo
8	187.5	10.8	991	2 I49540	procollagen C-endo
9	184.5	10.6	3623	2 T09456	intrinsic factor-B
10	174.5	10.0	1057	1 A39288	dorsal-ventral pat
11	172	9.9	3623	2 T08618	intrinsic factor-B
12	171.5	9.8	927	1 JQ0948	A5 antigen precurs
13	156.5	9.0	1524	2 T30337	polyprotein - Afri
14	151.5	8.7	1464	2 S58984	development protei
15	149	8.6	1070	2 T31069	tolloid-BMP-1 like
16	146.5	8.4	579	2 JC7629	membrane-type friz
17	146	8.4	686	1 A59271	Ra-reactive factor
18	141.5	8.1	767	2 T30018	hypothetical prote
19	138.5	8.0	1004	2 T30338	oviductin (EC 3.4.
20	138	7.9	2403	2 A59386	sanko - human
21	137.5	7.9	3871	2 T22812	hypothetical prote
22	137	7.9	276	2 A47290	TSG-6 homolog P84
23	136.5	7.8	449	2 A55362	procollagen I C-pr
24	135.5	7.8	699	1 I54763	Ra-reactive factor
25	133.5	7.7	597	2 S71352	metalloproteinase
26	130.5	7.5	402	2 JH0403	procollagen I C-pr
27	129	7.4	277	2 A41735	hyaluronate-bindin
28	127	7.3	705	1 C1HURB	complement subcomp
29	125.5	7.2	533	2 JC7985	brain-specific CUB

30	123.5	7.1	275	2 JC6506	tumor necrosis fac
31	122.5	7.0	1290	2 A57190	ebnerin precursor
32	121	6.9	419	2 S69207	vascular endotheli
33	120.5	6.9	321	2 T33161	hypothetical prote
34	120.5	6.9	333	2 T21595	hypothetical prote
35	120	6.9	695	1 S05008	complement subcomp
36	118.5	6.8	1034	1 A53663	enteropeptidase (E
37	116.5	6.7	688	1 C1HUS	complement subcomp
38	115.5	6.6	1594	2 T30549	hensin - rabbit
39	114.5	6.6	1019	1 A56318	enteropeptidase (E
40	114.5	6.6	1035	1 A43090	enteropeptidase (E
41	113	6.5	504	2 S56745	mucin (clone pGM31
42	113	6.5	694	2 JC6554	complement subcomp
43	112	6.4	555	2 T21028	hypothetical prote
44	112	6.4	2083	2 T42721	CRP-ductin-alpha p
45	112	6.4	2197	2 B71600	variant-specific s

ALIGNMENTS

RESULT 1

JC7591

spinal cord-derived growth factor-B precursor - human

C:Species: Homo sapiens (man)

C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004

C:Accession: JC7591

R:Hamada, T.; Ui-Tei, K.; Imaki, J.; Miyata, Y.

Biochem. Biophys. Res. Commun. 280, 733-737, 2001

A:Title: Molecular cloning of SCDGF-B, a novel growth factor homologous to SCDGF/PDGF-C/

A:Reference number: JC7591; MUID:21092670; PMID:11162582

A:Accession: JC7591

A:Molecule type: DNA

A:Residues: 1-370 <HAM>

A:Cross-references: UNIPROT:Q9BWV5; UNIPROT:Q9GZP0; DDBJ:AB033832

C:Genetics:

A:Gene: scdgf-B

F:1-17/Domain: secretory signal sequence #status predicted <SIG>

F:18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>

F:52-170/Region: CUB domain #status predicted

F:272-370/Region: homologous to platelet-derived growth factor/vascular endothelial growth

F:294-308/Region: conserved motif #status predicted

Query Match 99.7%; Score 1736; DB 2; Length 370;

Best Local Similarity 99.7%; Pred. No. 1.8e-127;

Matches 321; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LYRDETIQVKGNGYVQSPRPNLLLTWRLHSQENTRIQLVFDNQFGLAEANDI 60

Db 49 LYRDETIQVKGNGYVQSPRPNLLLTWRLHSQENTRIQLVFDNQFGLAEANDI 108

QY 61 CRYDFVEVEDISETSTIIRGWCHEVPRIKSRNQIKITFKSDDYFVAKPGFKIYYS 120

Db 109 CRYDFVEVEDISETSTIIRGWCHEVPRIKSRNQIKITFKSDDYFVAKPGFKIYYS 168

QY 121 LLEDQFAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDVDELLKYFN 180

Db 169 LLEDQFAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDVDELLKYFN 228

QY 181 PESWQEDLENMILDTPIRYGRSHDRKSKVDLRINDDAKRYSCTPRNSVNIREEKLKLA 240

Db 229 PESWQEDLENMILDTPIRYGRSHDRKSKVDLRINDDAKRYSCTPRNSVNIREEKLKLA 288

QY 241 NVVFPFCLLVQRCGNGCGGTNNWRSCTCNSGKTVKKYHEVLQFEPGHKRRGRAKTMA 300

Db 289 NVVFPFCLLVQRCGNGCGGTNNWRSCTCNSGKTVKKYHEVLQFEPGHKRRGRAKTMA 348

QY 301 LVDIQLDHHERCDCICSSRPPR 322

Db 349 LVDIQLDHHERCDCICSSRPPR 370

RESULT 2

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 29, 2004, 23:15:59 ; Search time 191 Seconds
(without alignments)
970.003 Million cell updates/sec

Title: US-10-086-623-6

Perfect score: 1742

Sequence: 1 LYRDETIQKGVQSPR.....DIQLDHHRCDCICSSRPPR 322

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt.02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1742	100.0	364	2	Q9BWV5	Q9bwv5 homo sapien
2	1742	100.0	364	2	AAQ89474	AAQ89474 homo sapi
3	1742	100.0	370	2	Q9GZP0	Q9gzp0 homo sapien
4	1567	90.0	370	2	Q9EQT1	Q9eqt1 rattus norv
5	1561	89.6	370	2	Q925I7	Q925i7 mus musculu
6	1493	85.7	300	2	Q6V9H4	Q6v9h4 oryctolagus
7	1493	85.7	300	2	AAQ24382	AAQ24382 oryctolag
8	965	55.4	261	2	Q8K2L3	Q8k2l3 mus musculu
9	751.5	43.1	345	2	Q9I946	Q9i946 gallus gall
10	750.5	43.1	345	2	Q9QY71	Q9qy71 m fallotein
11	748.5	43.0	345	2	Q8CI19	Q8ci19 mus musculu
12	742.5	42.6	345	2	Q9EQX6	Q9eqx6 rattus norv
13	740.5	42.5	345	2	Q9JH8	Q9jvh8 mus musculu
14	739.5	42.5	345	2	Q9UL22	Q9ul22 homo sapien
15	739.5	42.5	345	2	Q9NRA1	Q9nra1 homo sapien
16	739.5	42.5	345	2	AAQ88857	AAQ88857 homo sapi
17	632	36.3	258	2	Q8K429	Q8k429 rattus norv
18	189.5	10.9	707	1	BNP1_XENLA	P98070 xenopus lae
19	189.5	10.9	977	2	Q91925	Q91925 xenopus lae
20	188.5	10.8	735	2	Q57381	Q57381 xenopus lae
21	187.5	10.8	241	2	Q92135	Q92135 rattus norv
22	187.5	10.8	775	2	Q6P550	Q6p550 mus musculu
23	187.5	10.8	775	2	AAH63079	AAH63079 mus muscu
24	187.5	10.8	986	1	BNP1_HUMAN	P13497 homo sapien
25	187.5	10.8	991	1	BNP1_MOUSE	P98063 mus musculu
26	187.5	10.8	991	2	Q6NZM2	Q6nmz2 mus musculu
27	187.5	10.8	991	2	AAH66062	AAH66062 mus muscu
28	186.5	10.7	1015	2	Q9Y6L7	Q9y6l7 homo sapien
29	186.5	10.7	1078	2	Q9UQ00	Q9uq00 homo sapien
30	185	10.6	1007	2	Q6U128	Q6u128 xenopus lae
31	184.5	10.6	3494	2	Q7LC53	Q7lc53 homo sapien

32	184.5	10.6	3623	2	O60494	O60494 homo sapien
33	183.5	10.5	1012	2	Q9WVM6	Q9wvm6 mus musculu
34	180.5	10.4	1022	1	TLD_BRARE	O57460 brachydanio
35	177	10.2	954	2	Q75UQ6	Q75uq6 achaearanae
36	177	10.2	954	2	BAD01492	BAD01492 achaearan
37	175.5	10.1	309	2	Q6T495	Q6t495 brachydanio
38	175.5	10.1	309	2	AAR99509	AAR99509 brachydan
39	175.5	10.1	3620	2	Q9TUS3	Q9tus3 canis famli
40	175	10.0	871	2	Q6T869	Q6t869 brachydanio
41	175	10.0	871	2	AAR99506	AAR99506 brachydan
42	175	10.0	959	2	Q6T822	Q6t822 brachydanio
43	175	10.0	959	2	Q6T870	Q6t870 brachydanio
44	175	10.0	959	2	AAR89616	AAR89616 brachydan
45	175	10.0	959	2	AAR99505	AAR99505 brachydan

ALIGNMENTS

RESULT 1

Q9BWV5 PRELIMINARY; PRT; 364 AA.
 ID Q9BWV5
 AC Q9BWV5;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-OCT-2004 (Tremblrel. 28, Last annotation update)
 DE Iris-expressed growth factor short form (Platelet derived growth factor D, isoform 2) (SCDGF-B).
 GN Name=IEGF; Synonyms=PDGFD; ORFNames=UNQ1899;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RX MEDLINE=22103462; PubMed=12107412;
 RA Wistow G., Bernstein S.L., Ray S., Wyatt M.K., Behal A., Touchman J.W., Bouffard G., Smith D., Peterson K.;
 RA "Expressed sequence tag analysis of adult human iris for the NEIRBank project: steroid-response factors and similarities with retinal pigment epithelium";
 RL Mol. Vision 8:185-195 (2002).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Iris;
 RC MEDLINE=22388257; PubMed=12477932;
 RC TISSUE=Testis;
 RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., McQuellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Strausberg R.;
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]

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RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wicand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY027518; AAK20082.1; -.
DR EMBL; BC030645; AAH30645.1; -.
DR EMBL; AY359116; AAQ89474.1; -.
DR PIR; JC7591; JC7591.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR InterPro; IPR010916; TONB_Box_N.
DR Pfam; PF00431; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN 1.
SQ SEQUENCE 364 AA; 42166 MW; 245C53E8DDEA9EAC CRC64;

Query Match 100.0%; Score 1742; DB 2; Length 364;
Best Local Similarity 100.0%; Pred. No. 3e-129;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LYRRDETIQVKGNGYVQSPFPNSYPRLNLLTWRLHSQENTRIQLVFDNQFGLAEANDI 60
DB 43 LYRRDETIQVKGNGYVQSPFPNSYPRLNLLTWRLHSQENTRIQLVFDNQFGLAEANDI 102
QY 61 CRYDFVEVEDISSETTIIRGWCHEKVPPIKSRNQIKITFKSDDYFVAKPGFKIYYS 120
DB 103 CRYDFVEVEDISSETTIIRGWCHEKVPPIKSRNQIKITFKSDDYFVAKPGFKIYYS 162
QY 121 LLEDFQPAASATNWESVTSISGVSYNSPSVPTDPTLIADALDKKIAEFDVDELLKYFN 180
DB 163 LLEDFQPAASATNWESVTSISGVSYNSPSVPTDPTLIADALDKKIAEFDVDELLKYFN 222
QY 181 PESWQEDLENMYLDTPRYGRSYHDKRSKVDLRLNDLDAKRYSCPTPRNYSVNIREELKLA 240
DB 223 PESWQEDLENMYLDTPRYGRSYHDKRSKVDLRLNDLDAKRYSCPTPRNYSVNIREELKLA 282
QY 241 NVVFFPRCLLVORCGNGCGGVNWRSCVTKNSGKTVKKYHEVLQFEPGHIKRGRAKTM 300
DB 283 NVVFFPRCLLVORCGNGCGGVNWRSCVTKNSGKTVKKYHEVLQFEPGHIKRGRAKTM 342
QY 301 LVDIQLDHHERCDCICSSRPPR 322
DB 343 LVDIQLDHHERCDCICSSRPPR 364

RESULT 3
Q9GZP0 PRELIMINARY; PRT; 370 AA.
ID Q9GZP0
AC Q9GZP0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Spinal cord-derived growth factor-B (MSP036) (Platelet-derived growth
DE factor D) (Iris-expressed growth factor long form).
GN Name=hsCDGF-B; Synonyms=IEGF, PDGFD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21092670; PubMed=11162582;
RA Hamada T., Ui-Tel K., Imaki J., Miyata Y.;
RT "Molecular cloning of SCDF-B, a novel growth factor homologous to
RT SCDFG/PDGF-C/fallotein.";
RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RA Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S.,
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RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wicand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY027518; AAK20082.1; -.
DR EMBL; BC030645; AAH30645.1; -.
DR EMBL; AY359116; AAQ89474.1; -.
DR PIR; JC7591; JC7591.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR InterPro; IPR010916; TONB_Box_N.
DR Pfam; PF00431; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN 1.
SQ SEQUENCE 364 AA; 42166 MW; 245C53E8DDEA9EAC CRC64;

Query Match 100.0%; Score 1742; DB 2; Length 364;
Best Local Similarity 100.0%; Pred. No. 3e-129;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LYRRDETIQVKGNGYVQSPFPNSYPRLNLLTWRLHSQENTRIQLVFDNQFGLAEANDI 60
DB 43 LYRRDETIQVKGNGYVQSPFPNSYPRLNLLTWRLHSQENTRIQLVFDNQFGLAEANDI 102
QY 61 CRYDFVEVEDISSETTIIRGWCHEKVPPIKSRNQIKITFKSDDYFVAKPGFKIYYS 120
DB 103 CRYDFVEVEDISSETTIIRGWCHEKVPPIKSRNQIKITFKSDDYFVAKPGFKIYYS 162
QY 121 LLEDFQPAASATNWESVTSISGVSYNSPSVPTDPTLIADALDKKIAEFDVDELLKYFN 180
DB 163 LLEDFQPAASATNWESVTSISGVSYNSPSVPTDPTLIADALDKKIAEFDVDELLKYFN 222
QY 181 PESWQEDLENMYLDTPRYGRSYHDKRSKVDLRLNDLDAKRYSCPTPRNYSVNIREELKLA 240
DB 223 PESWQEDLENMYLDTPRYGRSYHDKRSKVDLRLNDLDAKRYSCPTPRNYSVNIREELKLA 282
QY 241 NVVFFPRCLLVORCGNGCGGVNWRSCVTKNSGKTVKKYHEVLQFEPGHIKRGRAKTM 300
DB 283 NVVFFPRCLLVORCGNGCGGVNWRSCVTKNSGKTVKKYHEVLQFEPGHIKRGRAKTM 342
QY 301 LVDIQLDHHERCDCICSSRPPR 322
DB 343 LVDIQLDHHERCDCICSSRPPR 364

RESULT 2
AAQ89474 PRELIMINARY; PRT; 364 AA.
ID AAQ89474
AC AAQ89474;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE SCDFG-B.
GN UNQ1899.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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RA Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,
RA Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.B., Wu Q.Y., Qiang B.Q.,
RA Xuan J.G., Liew C.C., Zhao M.S., Hui R.T.;
RN Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RP [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21231380; PubMed=11331882;
RA Lakochele W.J., Jeffers M., McDonald W.F., Chillakuru R.A.,
RA Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,
RA Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shimkets J.,
RA Shimkets R.A., Rothberg J.M., Lichenstein H.S.;
RT "PDGF D, A Novel Protease-Activated Growth Factor.";
RL Nat. Cell Biol. 3:517-521(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX PubMed=11331881;
RA Bergsten E., Uutela M., Li X., Pietras K., Ostman A., Heldin C.H.,
RA Alitalo K., Eriksson U.;
RT "PDGF-D is a specific, protease-activated ligand for the PDGF beta-
RT receptor.";
RL Nat. Cell Biol. 3:512-516(2001).
RN [5]
RP SEQUENCE FROM N.A.
RX TISSUE=Iris;
RC MEDLINE=22103462; PubMed=12107412;
RA Wistow G., Berstein S.L., Ray S., Wyatt M.K., Behal A., Touchman J.W.,
RA Bouffard G., Smith D., Peterson K.;
RT "Expressed sequence tag analysis of adult human iris for the NEIBank
RT Project: steroid-response factors and similarities with retinal
RT pigment epithelium";
RL Mol. Vision 8:185-195(2002).
DR EMBL; AB033832; BAB18903.1; -
DR EMBL; AF113216; AAG39287.1; -
DR EMBL; AF335584; AAK38840.1; -
DR EMBL; AF336376; AAK56136.1; -
DR EMBL; AY027517; AAK20081.1; -
DR PIR; JC7591; JC7591.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR InterPro; IPR010916; TONB_Box_N.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS02278; PDGF_2; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN 1.
SQ SEQUENCE 370 AA; 42848 MW; D387F485E7BB7674_CRC64;

Query Match 100.0%; Score 1742; DB 2; Length 370;
Best Local Similarity 100.0%; Pred. No. 3.1e-129;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LYRDETIQKNGYGVQSPFPNSYPNLLTWRHLSQENTRIQLVFNQFGLSEAENDI 60
Db 49 LYRDETIQKNGYGVQSPFPNSYPNLLTWRHLSQENTRIQLVFNQFGLSEAENDI 108

Qy 61 CRYDFVEVEDISESTTIIRGWCCHKEVPPRIKSRNTQIKITFKSDDDYFVAKPGFKIYYS 120
Db 109 CRYDFVEVEDISESTTIIRGWCCHKEVPPRIKSRNTQIKITFKSDDDYFVAKPGFKIYYS 168

Qy 121 LLEDFQPAASSETNWESVTSISGVSYNSPSVTDPTLADALDKKIAEFDTVEDLLKYFN 180
Db 169 LLEDFQPAASSETNWESVTSISGVSYNSPSVTDPTLADALDKKIAEFDTVEDLLKYFN 228

Qy 181 PESWQEDLENMYLDTPRYGRSHYDRKSKVDLDRNLDDAKRYSCPTPRNYSVNIREELKLA 240
Db 229 PESWQEDLENMYLDTPRYGRSHYDRKSKVDLDRNLDDAKRYSCPTPRNYSVNIREELKLA 288

Qy 241 NVVFPFRCLLVQRCGNGCGGTNNRSCTCNSGKTVKKYHEVLQEPGHIKRRGAKTMA 300
Db 241 NVVFPFRCLLVQRCGNGCGGTNNRSCTCNSGKTVKKYHEVLQEPGHIKRRGAKTMA 300

Db 289 NVVFPFRCLLVQRCGNGCGGTNNRSCTCNSGKTVKKYHEVLQEPGHIKRRGAKTMA 348
Qy 301 LVDIQLDHHERCDCICSSRPPR 322
Db 349 LVDIQLDHHERCDCICSSRPPR 370

RESULT 4
ID Q9EQTI PRELIMINARY; PRT; 370 AA.
AC Q9EQTI;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Spinal-cord derived growth factor-B.
GN Name=rSCDGF-B;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21092670; PubMed=11162582;
RA Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
RT "Molecular cloning of SCDGF-B, a novel growth factor homologous to
RT SCDGF/PDGF-C/fallotin.";
RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
DR EMBL; AB052170; BAB18920.1; -
DR PIR; JC7592; JC7592.
DR HSP; Q9UCV4; INZI.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS02278; PDGF_2; 1.
SQ SEQUENCE 370 AA; 42809 MW; 7BE8A251F679BF73_CRC64;

Query Match 90.0%; Score 1567; DB 2; Length 370;
Best Local Similarity 87.0%; Pred. No. 2.1e-115;
Matches 280; Conservative 22; Mismatches 20; Indels 0; Gaps 0;

Qy 1 LYRDETIQKNGYGVQSPFPNSYPNLLTWRHLSQENTRIQLVFNQFGLSEAENDI 60
Db 49 LYRDETIQKNGYGVQSPFPNSYPNLLTWRHLSQENTRIQLVFNQFGLSEAENDI 108

Qy 61 CRYDFVEVEDISESTTIIRGWCCHKEVPPRIKSRNTQIKITFKSDDDYFVAKPGFKIYYS 120
Db 109 CRYDFVEVEDISESTTIIRGWCCHKEVPPRIKSRNTQIKITFKSDDDYFVAKPGFKIYYS 168

Qy 121 LLEDFQPAASSETNWESVTSISGVSYNSPSVTDPTLADALDKKIAEFDTVEDLLKYFN 180
Db 169 LLEDFQPAASSETNWESVTSISGVSYNSPSVTDPTLADALDKKIAEFDTVEDLLKYFN 228

Qy 181 PESWQEDLENMYLDTPRYGRSHYDRKSKVDLDRNLDDAKRYSCPTPRNYSVNIREELKLA 240
Db 229 PESWQEDLENMYLDTPRYGRSHYDRKSKVDLDRNLDDAKRYSCPTPRNYSVNIREELKLA 288

Qy 241 NVVFPFRCLLVQRCGNGCGGTNNRSCTCNSGKTVKKYHEVLQEPGHIKRRGAKTMA 300
Db 289 NAVFPFRCLLVQRCGNGCGGTNNRSCTCNSGKTVKKYHEVLQEPGHIKRRGAKTMA 348

Qy 301 LVDIQLDHHERCDCICSSRPPR 322
Db 349 LVDIQLDHHERCDCICSSRPPR 370

RESULT 5
Q92517

Q925I7 PRELIMINARY; PRT; 370 AA.
AC Q925I7; Q9D1L8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Placlet-derived growth factor D (Mus musculus 18-day embryo whole
DE body cDNA, RIKEN full-length enriched library, clone:110003109
DE product:platelet-derived growth factor D).
GN Name=PDGf;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=21231380; PubMed=11331882;
RA LaRoche W.J., Jeffers M., McDonald W.F., Chillakuru R.A.,
RA Giese N.A., Lokker N.A., Sullivan C., Boldog F.B., Yang M., Vernet C.,
RA Burgess C.B., Fernandez E., Deegler L.L., Rittman B., Shinkets J.,
RA Shinkets R.A., Rothberg J.M., Lichenstein H.S.;
RT "PDGF D, A Novel Protease-Activated Growth Factor";
RL Nat. Cell Biol. 3:517-521 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=9927253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning";
RL Meth. Enzymol. 303:19-44 (1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690 (2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes";
RN Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes";
RN Genome Res. 10:1617-1630 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer";
RL Genome Res. 10:1757-1771 (2000).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861;
RA Aizawa K., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Teijima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF335583; AAK38839.1; -;
DR EMBL; AK003359; BAB22735.2; -;
DR MGD; MGI:1919035; PDGf.
DR GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphorylation; IDA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS02078; PDGF 2; 1.
SQ SEQUENCE 370 AA; 42809 MW; 9E80B4CF6813BFBE CRC64;
Query Match 89.6%; Score 1561; DB 2; Length 370;
Best Local Similarity 86.6%; Pred. No. 6.1e-115;
Matches 279; Conservative 23; Mismatches 20; Indels 0; Gaps 0;
QY 1 LVRRDETQVKGNGVQSPFPNSVPRNLLLTWRLHSEENTRIQLVFDNQFGLAEANDI 60
DB 49 LYQRENIQVTSNGHVQSPFPNSVPRNLLLTWRLHSEENTRIQLVFDNQFGLAEANDI 103
QY 61 CRYDFVEVEDISSTIIRGWCGRKEVPPRIKRTNQIKITFKSDDYFVAKPGKIYYS 120
DB 109 CRYDFVEVEVESSTVVRGWCGRKEVPPRIKRTNQIKITFKSDDYFVAKPGKIYYS 163
QY 121 LLEDPQAAASSETWESVTSISGVSNYSVPTDPTLIADALDKKIAEDFVDELKYN 180
DB 169 FVEDFQPEAASETWESVTSISGVSNYSVPTDPTLIADALDKKIAEDFVDELKYN 228
QY 181 PESQOEDLENMYLDTPRYGRGSHDRKSKVDLDRNDLNDKAYSCTPRNVNIREELKIA 240
DB 229 PVSQWQDLENLYLDTPHYRGSHYDRKSKVDLDRNDLNDKAYSCTPRNVNIREELKLT 288
QY 241 NVVFPFRCLLVQRCGNGCGCTVNRSCVTKYKHYVLPQEPGHIKRRGAKTMA 300
DB 289 NAVFPFRCLLVQRCGNGCGCTVNRSCVTKYKHYVLPQEPGHIKRRGAKTMA 348
QY 301 LVDQLDHHRCDCICSSRRPR 322
DB 349 LVDQLDHHRCDCICSSRRPR 370
RESULT 6
Q6V9H4 PRELIMINARY; PRT; 300 AA.
AC Q6V9H4;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Iris-expressed growth factor (Fragment).
GN Name=PDGf;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Ray S., Wistow G.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY347260; AAQ24382.1; -;
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.

DR SMART: SM00042; CUB: 1.
DR PROSITE; PS01180; CUB: 1.
DR PROSITE; PS0278; PDGF 2; 1.
FT NON_TER 1 1
FT NON_TER 300 300
SQ SEQUENCE 300 AA; 34616 MW; 716C873C9C01C0C6 CRC64;

Query Match 85.7%; Score 1493; DB 2; Length 300;
Best Local Similarity 91.3%; Pred. No. 1.1e-109;
Matches 274; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

QY 9 QVKGNGYVQSPFPNSYPRLNLLTWRLHSEQENTRIQLVFDNQFGLAEAEENDICRYDFVEV 68
DB 1 QVTGNHGVQSLAAPPNSYPRLNLLTWRLHSEQENTRIQLVFDNQFGLAEAEENDICRYDFVEV 60

QY 69 EDISSTIIRGRWCGHKEVPPRIKSRNQIKITPKSDDYFVAKPGFKIYYSLLDFDQFA 128
DB 61 EDISSTVIRGRWCGHKEVPPRIKSRNQIKITPKSDDYFVAKPGFKIYYSFVDFDQFA 120

QY 129 AASNTWESVTSSISGVSNPSVTDPTLIADLKKIAEFDTVEDLLKYNPESWQBDL 188
DB 121 AASNTWESVTSSISGVSNPSVTDPTLIADLKKIAEFDTVEDLLKYNPESWQBDL 180

QY 189 ENMYLDTPRYGRSVHDKRSKVDLRLNDADAKRYSCPTPNYSVNIREEKLKLVVFFPRC 248
DB 181 ENMYLDTPRYGRSVHDKRSKVDLRLNDADAKRYSCPTPNYSVNIREEKLKLVVFFPRC 240

QY 249 LLVQRCGCGCGTNNWRSCTNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDH 308
DB 241 LLVQRCGCGCGTNNWRSCTNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDH 300

RESULT 7
AAQ24382 PRELIMINARY; PRT; 300 AA.
AC AAQ24382
DT 02-MAR-2004 (TRENBLrel. 27, Created)
DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TRENBLrel. 27, Last annotation update)
DE Iris-expressed growth factor (Fragment).
GN PDGFD.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Ray S., Wistow G.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY347260; AAQ24382.1; -.
FT NON_TER 1 1
FT NON_TER 300 300
SQ SEQUENCE 300 AA; 34616 MW; 716C873C9C01C0C6 CRC64;

Query Match 85.7%; Score 1493; DB 2; Length 300;
Best Local Similarity 91.3%; Pred. No. 1.1e-109;
Matches 274; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

QY 9 QVKGNGYVQSPFPNSYPRLNLLTWRLHSEQENTRIQLVFDNQFGLAEAEENDICRYDFVEV 68
DB 1 QVTGNHGVQSLAAPPNSYPRLNLLTWRLHSEQENTRIQLVFDNQFGLAEAEENDICRYDFVEV 60

QY 69 EDISSTIIRGRWCGHKEVPPRIKSRNQIKITPKSDDYFVAKPGFKIYYSLLDFDQFA 128
DB 61 EDISSTVIRGRWCGHKEVPPRIKSRNQIKITPKSDDYFVAKPGFKIYYSFVDFDQFA 120

QY 129 AASNTWESVTSSISGVSNPSVTDPTLIADLKKIAEFDTVEDLLKYNPESWQBDL 188
DB 121 AASNTWESVTSSISGVSNPSVTDPTLIADLKKIAEFDTVEDLLKYNPESWQBDL 180

QY 189 ENMYLDTPRYGRSVHDKRSKVDLRLNDADAKRYSCPTPNYSVNIREEKLKLVVFFPRC 248
DB 181 ENMYLDTPRYGRSVHDKRSKVDLRLNDADAKRYSCPTPNYSVNIREEKLKLVVFFPRC 240

QY 249 LLVQRCGCGCGTNNWRSCTNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDH 308
DB 241 LLVQRCGCGCGTNNWRSCTNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDH 300

RESULT 8
Q8K2L3 PRELIMINARY; PRT; 261 AA.
AC Q8K2L3
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE PDGfd protein.
GN Name=PDGfd;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=FVB/N;
RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy.;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Altschul S.F., Zeeb B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N;
RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy.;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030896; AAH30896.1; -.
DR MGD; MGI:1919035; PDGfd.
DR GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. . ; IDA.
DR InterPro; IPR000859; CUB.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
SQ SEQUENCE 261 AA; 30228 MW; 2EEC3F6373A52D09 CRC64;

Query Match 85.4%; Score 965; DB 2; Length 261;
Best Local Similarity 54.2%; Pred. No. 4.7e-68;
Matches 176; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

QY 1 LYRDEITQVKGNGYVQSPFPNSYPRLNLLTWRLHSEQENTRIQLVFDNQFGLAEAEENDI 60
DB 49 LYRDEENITQVKGNGYVQSPFPNSYPRLNLLTWRLHSEQENTRIQLVFDNQFGLAEAEENDI 108

QY 61 CRYDFVEDEIVSETTIIRGRWCGHKEVPPRIKSRNQIKITPKSDDYFVAKPGFKIYYS 120
DB 109 CRYDFVEVEEVSESTVIRGRWCGHKEVPPRIKSRNQIKITPKSDDYFVAKPGFKIYYS 168

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QY 121 LLEDQPAASATNWSVTSSISGVNSPSTVDPTLTADALDKKIARFDTVEDLLKYFN 180
Db 169 FVEDSQPAASATNWSVTSSISGVNSPSTVDPTLTADALDKKIARFDTVEDLLKHFN 228

QY 181 PESWQEDLENMYLDTPRYGRSRYHDKRSK 209
Db 229 PYSWQDDLENLYDTPHYGRSRYHDKRSK 257

RESULT 9
Q91946 PRELIMINARY; PRT; 345 AA.
AC Q91946;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE Spinal cord-derived growth factor.
GN Name=SCDGF;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=white leghorn; TISSUE=Spinal cord;
RX MEDLINE=20317014; PubMed=10858496;
RA Hamada T., Ui-Rei K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDGF, is a unique member of the PDGF/VBGF family.";
RL FEBS Lett. 475:97-102(2000).
CC 1- SIMILARITY: Belongs to the PDGF/VBGF growth factor family.
DR EMBL; AB033829; BAB03265.1; -.
DR HSSP; Q9UCV4; INZI.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Growth factor; Mitogen.
SQ SEQUENCE 345 AA; 38940 MW; 97ACEA992BF5128C CRC64;

Query Match 43.1%; Score 751.5; DB:2; Length 345;
Best Local Similarity 47.0%; Pred. No. 5e-51;
Matches 150; Conservative 53; Mismatches 87; Indels 29; Gaps 8;

QY 3 RDEDTQKNGVQSPRPNFNSYPRNLLTWRHS-OENTRIQLVPDNOFGLEEAENDIC 61
Db 45 QHEKIITVTSNGSIHSPKPTHTYPRNTVLVAVDENWVIQLTDERFGLDEPDDIC 104

QY 62 RYDFVEVEDISESTIIRGRWCCHKVPRIKRSTNQIKTKSDDYFVAKPGFKIYSL 121
Db 105 KYDFVEVEPSDGTVL--GRWCSSSVPSRQSKGNQIRFVSDSYFFSPGFCIHYTL 162

QY 122 LEDQPAASATNWSVTSSISGVNSPSTVDPT-LIADALDKKIARFDTVEDLLKYFN 180
Db 163 LVPHTTEAP-----SPSSLPPSALPLDLVNNVAGFSTVEELIRYLE 204

QY 181 PESWQEDLENMYLDTPRYGRSRYHDKRSK-VLDRLNDADKRYSTPRNYSVNIIEELK 238
Db 205 PDRWQLDLEDYRPTWQLLKAYIHGKRSRVLDNLKKEEVRLYSTPRNFSVSLIEELK 264

QY 239 LANVWFFPRCLLVORCGNCGCTVNWRSCTNSGKTVKYHEVLOFEPGHIKRRG-RAK 297
Db 265 RTDTIFWPLCLLVKRCGNCACCHQNCNEQCIPTKVKYHEVLOLKP-----RSGVRGL 320
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QY 298 TMALVDIQLDHHRCDCIC 316
Db 321 HKSITDPLFHEHSCDCVC 339

RESULT 10
Q9QY71 PRELIMINARY; PRT; 345 AA.
AC Q9QY71;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE Fallotein (Platelet-derived growth factor C) (Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130403008 product:platelet-derived growth factor, C polypeptide, full insert sequence) (Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730022G11 product:platelet-derived growth factor, C polypeptide, full insert sequence) (Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930001M08 product:platelet-derived growth factor, C polypeptide, full insert sequence).
GN Name=Pdgfc;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Tsai Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Gao Z., Hart C., Piddington C., Sheppard P., Shoemaker K., Gilbertson D., West J., O'Hara P.J.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RA The FANTOM Consortium;
RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
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Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sugi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multiplex capillary sequencer"; Genome Res. 10:1757-1771 (2000).
[8]
SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
Aadachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Koijima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y., Saito R., Saibata H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sugabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
- !- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
EMBL; AF117608; AAF22516.1; -
EMBL; AF266467; AAKS8566.1; -
EMBL; AK033734; BAC28455.1; -
EMBL; AK042767; BAC31359.1; -
EMBL; AK052947; BAC35216.1; -
MGI; MG1:1859631; Pdgifc.
GO; GO:0005576; C:extracellular; IDA.
GO; GO:0005163; P:platelet-derived growth factor receptor bin. ; IDA.
GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. ; IDA.
GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. ; IDA.
InterPro; IPRO00859; CUB.
InterPro; IPRO00072; PD_growth_factor.
Pfam; PF00431; CUB; 1.
Pfam; PF00341; PDGF; 1.
SMART; SM00042; CUB; 1.
SMART; SM00141; PDGF; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS02078; PDGF 2; 1.
Growth factor; Mitogen.
SEQUENCE 345 AA; 38741 MW; 3A58A1F701B84EA2 CRC64;
Query Match 43.1%; Score 750.5; DB 2; Length 345;
Best Local Similarity 45.6%; Pred. No. 6e-51;
Matches 145; Conservative 58; Mismatches 88; Indels 27; Gaps 8
QY 3 RDETIQVKGNGYQVSPPPNYSYRNLLLTWRLLHS-QENTRIOLVDNQFGLEAEANDIC 61
DB 45 RHRRVVTTISGNGSHSPFPHTYPRNMVLVRWLVAVDENVRIQLTDFERGLDEPDDIC 104
QY 62 RYDFVEVEDISETSTIRGRWCGHKEPVPRPKSRRTNOIKITFKSDDYFVAKPGFKIYYSL 121
DB 105 KYDFVEVEPSDGSVL--GRWCSGSTVGKTSKGNHIRRFVSDYDFSEFGFCIHYSI 162
QY 122 LEDFOFAAASETNWESVTSSISGVSYNSPYTDP-TLIAADALDKKIABFTDVEDLLKYPN 180
DB 163 I---MPQVTEIT-----SPSVLPSSLSDLNNNAVTAFTAEELIRYLE 204
QY 181 PESWQEDLENMVLDTPRYGRBSY-HDRKSK-VDLDRNLDDAKKYSCCTPNYSYNVIREELK 238
DB 205 PDRWQQLDLSLYKPTQWLLGKAFLGYKKSKVNNILLKEEVKLTYCSTPRNFVSIREELK 264
QY 239 LANVVFPPRCLLIVQRCCGNCGGTWNRSCTCSGKTWKYKHVEVLOFEPGHIKRRGRAKT 298
DB 265 RTDTTFWPCCLLVKRCGNCACCLHCNCEOCVPKRKYKXHEVLQLRP----KTGVKGLH 321
QY 299 MALVDIQLDHHHRCDIC 316

Db 322 KSLTVDALHHBECDCVC 339

RESULT 11

Q8C119 PRELIMINARY; PRT; 345 AA.

ID Q8C119

AC Q8C119; 01-MAR-2003 (TEMBLrel. 23, Created)

DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)

DE Platelet-derived growth factor, C polypeptide.

GN Name=PDGf;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CZECH II;

RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model;

RC Expression driven by an MMTV-LTR enhancer.;

RX MEDLINE=223488257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Rapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.J., Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grichman J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywicki M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=CZECH II;

RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.

RC Expression driven by an MMTV-LTR enhancer.;

RA Strausberg R.

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.

EMBL BC037696; AAH37696.1; -.

DR MGD; MGI:1859631; Pdgfc.

DR GO; GO:0005576; C:extracellular; IDA.

DR GO; GO:0005161; F:platelet-derived growth factor receptor bin..; IDA.

DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.

DR GO; GO:0007380; P:regulation of peptidyl-tyrosine phosphoryla..; IDA.

DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin..; IDA.

DR InterPro; IPR000859; CUB.

DR InterPro; IPR000072; PD_growth_factor.

DR Pfam; PF00431; CUB; 1.

DR Pfam; PF00341; PDGF; 1.

DR SMART; SM00042; CUB; 1.

DR SMART; SM00141; PDGF; 1.

DR PROSITE; PS01180; CUB; 1.

DR PROSITE; PS0278; PDGF_2; 1.

DR Growth factor; Mitogen.

QY SEQUENCE 345 AA; 38741 MW; 9A58A05C6C0E9614 CRC64;

Query Match 43.0%; Score 748.5; DB 2; Length 345;

Best Local Similarity 45.3%; Pred.No. 8.6e-51;

Matches 144; Conservative 59; Mismatch 88; Indels 27; Gaps

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Db 45 RHERVVTISGNGSIHSPKPHYPRNMVLRVAVDENVRILQITDFERFGLDEPDDLC 104
Qy 62 RYDFVEVEDISTYIRGWCCHKEVPPRIKSRNQIKITFKSDDYFVAKPGFKIYSL 121
Db 105 KYDFVEVEEPPSDGSL--GRWCGSGTVPGKQTSKGNHIRIRFVSDYFPPSPGFCIHYSI 162
Qy 122 LEDFOQAAASATNWESVTSSISGVSYNSPSVTPD-TLIAADLKKIAEFTDVEDLLKYFN 180
Db 163 I---MPQVTTT-----SPSVLPSSLSLDLNNAVATFSTVEELIRYLE 204
Qy 181 PESWOEDLENMYLDTPRYGRSY-HDRKSK-VDLRLNDDAKRYSCPTPNYSVNIREEK 238
Db 205 PDRWQVDLSLYKPTWQLLGAFLYKSKAVNLLKEEVKLYSCTPRNFSVSIREELK 264
Qy 239 LANVVFPRCLLVQRCGNGCGTVNWRSCNCSKTKVKKYHEVLOFEPGHIKRRGRAT 298
Db 265 RTDTIFWPGCLLVKRCGNGCACCLHNCQCQVPRKVTKKYHEVLOLRP---KTGVKGLH 321
Qy 299 MALVDIQLDHERCDIC 316
Db 322 KSLTDVALEHHEECDCVC 339

RESULT 12
Q9EQX6 PRELIMINARY; PRT; 345 AA.
AC Q9EQX6;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Spinal cord-derived growth factor.
GN Name=Scdgl;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP STRAIN=Swiss-Webster;
RC STRAIN=Swiss-Webster;
RX MEDLINE=21092670; PubMed=11162582;
RA Hamada T., Ui-Tei K., Inaki J., Miyata Y.;
RT "Molecular cloning of SCDF-B, a novel growth factor homologous to
RL SCDF/PDGF-C/fallotin."
RC Biochem. Biophys. Res. Commun. 280:733-737(2001).
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0008083; P-growth factor activity; IEA.
DR GO; GO:0008151; P-cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR Pfam; PF00431; PDGF; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Growth factor; Mitogen.
SQ SEQUENCE 345 AA; 38734 MW; F296DA6E9B765D10 CRC64;
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Query Match 42.6%; Score 742.5; DB 2; Length 345;
Best Local Similarity 45.6%; Pred. No. 2.6e-50;
Matches 145; Conservative 59; Mismatches 87; Indels 27; Gaps 9;

Qy 3 RRETIQVKGNGYVQSPFPNSYPNLLTWRLHS-QENTRIQLVDFNQGLEAENDIC 61
Db 45 RHERVVTISGNGSIHSPKPHYPRNMVLRVAVDENVRILQITDFERFGLDEPDDLC 104
Qy 62 RYDFVEVEDISTYIRGWCCHKEVPPRIKSRNQIKITFKSDDYFVAKPGFKIYSL 121
Db 105 KYDFVEVEEPPSDGSL--GRWCGSGTVPGKQTSKGNHIRIRFVSDYFPPSPGFCIHYSI 162
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Qy 122 LEDFOQAAASATNWESVTSSISGVSYNSPSVTPD-TLIA-DALDKKIAEFTDVEDLLKYFN 180
Db 163 I---MPQVTTT-----SPSVLPSSLSLDLNNAVATFSTVEELIRYLE 204
Qy 181 PESWOEDLENMYLDTPRYGRSY-HDRKSK-VDLRLNDDAKRYSCPTPNYSVNIREEK 238
Db 205 PDRWQVDLSLYKPTWQLLGAFLYKSKAVNLLKEEVKLYSCTPRNFSVSIREELK 264
Qy 239 LANVVFPRCLLVQRCGNGCGTVNWRSCNCSKTKVKKYHEVLOFEPGHIKRRGRAT 298
Db 265 RTDTIFWPGCLLVKRCGNGCACCLHNCQCQVPRKVTKKYHEVLOLRP-KIGVKGLHK- 322
Qy 299 MALVDIQLDHERCDIC 316
Db 323 -SLTDVALEHHEECDCVC 339

RESULT 13
Q9JHV8 PRELIMINARY; PRT; 345 AA.
AC Q9JHV8;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Platelet-Derived growth factor C.
GN Name=PDGfc;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss-Webster;
RX MEDLINE=20417814; PubMed=10960785;
RA Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;
RT "The mouse Pdgfc gene: dynamic expression in embryonic tissues during
RT organogenesis."
RL Mech. Dev. 96:209-213(2000).
DR EMBL; AF286725; AAF91483.1; -.
DR MGD; MGI:1859631; Pdgfc.
DR GO; GO:0005576; C-extracellular; IDA.
DR GO; GO:0005161; P-platelet-derived growth factor receptor bin. .; IDA.
DR GO; GO:0008284; P-positive regulation of cell proliferation; IDA.
DR GO; GO:0050730; P-regulation of peptidyl-tyrosine phosphoryla. .; IDA.
DR GO; GO:0007171; P-transmembrane receptor protein tyrosine kin. .; IDA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
SQ SEQUENCE 345 AA; 38886 MW; FA1486BED6D362F8 CRC64;
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Query Match 42.5%; Score 740.5; DB 2; Length 345;
Best Local Similarity 45.3%; Pred. No. 3.7e-50;
Matches 144; Conservative 58; Mismatches 89; Indels 27; Gaps 8;

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Db 105 KYDFVEVEEPPSDGSL--GRWCGSGTVPGKQTSKGNHIRIRFVSDYFPPSPGFCIHYSI 162
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DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
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RC Tissue=Uterus;
RX MEDLINE=20461776; PubMed=11004490;
RA Tsai Y.J., Lee R.K., Lin S.P., Chen Y.H.;
RT "Identification of a novel platelet-derived growth factor-like gene, fallotain, in the human reproductive tract.";
RL Biochim. Biophys. Acta 1492:196-202(2000).
RN [2];
RP SEQUENCE FROM N.A.
RC Tissue=Brain;
RX MEDLINE=20317014; PubMed=10858496;
RA Hamada T., Ui-Tei K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDGF, is a unique member of the PDGF/VEGF family.";
RL FEBS Lett. 475:97-102(2000).
RN [3];
RP SEQUENCE FROM N.A.
RX MEDLINE=21347863; PubMed=11297552;
RA Gilbertson D.G., Durf M.E., West J.W., Kelly J.D., Sheppard P.O., Hofstrand P.D., Gao Z., Shoemaker K., Bukowski T.R., Moore M., Feidhaus A.L., Humes J.M., Palmer T.E., Hart C.E.;
RT "Platelet-derived growth factor C (PDGF-C), a novel growth factor that binds to PDGF alpha and beta receptor.";
RL J. Biol. Chem. 276:27406-27414(2001).
RN [4];
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Kilmadi C., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Weand D., Woods K., Xie M.H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AF091434; AAF00049.1; -;
DR EMBL; AB033831; BAB03266.1; -;
DR EMBL; AF260738; AAK51637.1; -;
DR EMBL; AY358493; AAQ8857.1; -;
DR GO; GO:000576; C:extracellular; NAS.
DR GO; GO:0008083; F:growth factor activity; TAS.
DR GO; GO:0007417; F:central nervous system development; TAS.
DR InterPro; IPR000859; CUB.

DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
SQ SEQUENCE 345 AA; 39029 MW; CDE9E51F40633E78 CRC64;
Query Match 42.5%; Score 739.5; DB 2; Length 345;
Best Local Similarity 47.0%; Pred. No. 4.4e-50;
Matches 150; Conservative 51; Mismatches 89; Indels 29; Gaps 8;
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DB 204 EPERWQLDLEDLYRPTWLLGKAFVFGKRKSRVDNLNLTTEVRLYSCTPRNFSVIREEL 263
QY 238 KLANVVFPRCLLVQRCGCGCGTWNRSCTCNCKTKVKKHEVLQFEPGHIKRRGRAK 297
DB 264 KRTDTIFWPGCLLVKRCGCGCACCLHCNECCQVPSKVKYKHEVLQLRP---KTGVRGL 320
QY 298 TMAVLDIQLDHHERCDCIC 316
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AC Q9NRAI;
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DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Platelet-derived growth factor C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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RP SEQUENCE FROM N.A.
RC Tissue=Lung;
RX MEDLINE=20268201; PubMed=10806482;
RA Li X., Ponten A., Aase K., Karlsson L., Abramson A., Urtela M., Backstrom G., Hellstrom M., Bostrom H., Li H., Soriano P., Besholtz C., Heidlin C.-H., Alitalo K., Ostman A., Eriksson U.;
RT "PDGF-C is a new protease-activated ligand for the PDGF alpha-receptor.";
RL Nat. Cell Biol. 2:302-309(2000).
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AF244813; AAF80597.1; -;
DR Genbank; HGNC:8801; PDGFC.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR Growth factor; Mitogen.

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OM nucleic - nucleic search, using sw model

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Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	1491.8	77.1	1882	4	US-09-564-595D-1
6	1491.8	77.1	1882	4	US-09-706-968-36
7	1491.8	77.1	1882	4	US-09-808-972-1
8	1003.4	51.9	1162	4	US-10-140-002-185
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42	63	3.0	452	4	US-09-621-976-1352	Sequence 1352, Appl
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ALIGNMENTS

RESULT 1
US-09-438-046-5
; Sequence 5, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTN, Annica
; APPLICANT: UTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D,
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; CURRENT FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; EARLIER FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1934
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(966)
US-09-438-046-5

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1934; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; CURRENT FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10

EARLIER APPLICATION NUMBER: 60/113,997
EARLIER FILING DATE: 1999-12-28
EARLIER APPLICATION NUMBER: 60/150,604
EARLIER FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: 60/157,108
EARLIER FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: 60/157,756
EARLIER FILING DATE: 1999-10-05
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7

LENGTH: 2253

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (176)..(1288)

US-09-438-046-7

Query Match 100.0%; Score 1934; DB 4; Length 2253;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1934; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TTGTACCGAAGATGAGACATCCAGGTGAAGGAACGGCTACGTCAGAGTCCTAGA	60
Db	320	TTGTACCGAAGATGAGACATCCAGGTGAAGGAACGGCTACGTCAGAGTCCTAGA	379
Qy	61	TTCCGGAACAGTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGAGAAAT	120
Db	380	TTCCGGAACAGTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGAGAAAT	439
Qy	121	ACCGGATACAGTACGTTGTTGACAAATCAGTTGGATTAGAGGAGCAAGAAATGATATC	180
Db	440	ACCGGATACAGTACGTTGTTGACAAATCAGTTGGATTAGAGGAGCAAGAAATGATATC	499
Qy	181	TGTAGGTATGATTTTGTGGAGTTGAAGATATATCCGGAACAGTACCAATATTAGAGGA	240
Db	500	TGTAGGTATGATTTTGTGGAGTTGAAGATATATCCGGAACAGTACCAATATTAGAGGA	559
Qy	241	CGATGGTGGACACAGGAAGTTCCCTCAAGGATAAAATCAAGAACCAACCAAAATATA	300
Db	560	CGATGGTGGACACAGGAAGTTCCCTCAAGGATAAAATCAAGAACCAACCAAAATATA	619
Qy	301	ATCATTCAAGTCGGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTATTATTCT	360
Db	620	ATCATTCAAGTCGGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTATTATTCT	679
Qy	361	TTGCTGGAAGATTTCACACCCGACAGGTTTCAGAGACCAATGGGAATCTGTCAAGC	420
Db	680	TTGCTGGAAGATTTCACACCCGACAGGTTTCAGAGACCAATGGGAATCTGTCAAGC	739
Qy	421	TCTATTTCAGGGGTATCCTATAACTCTCCATCAGTAACGGATCCCACTCTGATTGCGGAT	480
Db	740	TCTATTTCAGGGGTATCCTATAACTCTCCATCAGTAACGGATCCCACTCTGATTGCGGAT	799
Qy	481	GCTCTGGACAAAAAATTCAGAAATTTGATACAGTGGGAAGATCTGCTCAAGTACTTCAAT	540
Db	800	GCTCTGGACAAAAAATTCAGAAATTTGATACAGTGGGAAGATCTGCTCAAGTACTTCAAT	859
Qy	541	CCAGAGTCAATGCAAGAGATCTTGAAGATATGATCTTGGACACCCCTCGGTATCGAGGC	600
Db	860	CCAGAGTCAATGCAAGAGATCTTGAAGATATGATCTTGGACACCCCTCGGTATCGAGGC	919
Qy	601	AGGTATACCATGACCGGAGTCAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG	660
Db	920	AGGTATACCATGACCGGAGTCAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG	979
Qy	661	CGTTACAGTTGACCTCCAGGAATTTACTCGGTCAATATAAGAGAGAGCTGAAGTTGGCC	720
Db	980	CGTTACAGTTGACCTCCAGGAATTTACTCGGTCAATATAAGAGAGAGCTGAAGTTGGCC	1039
Qy	721	AATGTGGTCTCTTTCCAGTTCCTCTCTGTCAGCGCTGTGGAGGAATTTGTGGCTGT	780

Db	1040	AATGTGGTCTCTTTCCACGTTGCCCTCCTCGTGCAGCGCTGTGGAGGAAATTTGTGGCTGT	1099
Qy	781	GGAACTCTCAACTGGAGGTCTCTGCACATGCAATTCAGGGAAAAACCGTGAAGATATCAT	840
Db	1100	GGAACTCTCAACTGGAGGTCTCTGCACATGCAATTCAGGGAAAAACCGTGAAGATATCAT	1159
Qy	841	GAGGTATTACAGTTTGAGCTGGCCACATCAAGAGGAGGGGTAGAGCTAGACCATGGCT	900
Db	1160	GAGGTATTACAGTTTGAGCTGGCCACATCAAGAGGAGGGGTAGAGCTAGACCATGGCT	1219
Qy	901	CTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTGTATCTGCAGCTCAAGACCA	960
Db	1220	CTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTGTATCTGCAGCTCAAGACCA	1279
Qy	961	CCTCGATAAGAGAAATGTCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTAGAGGA	1020
Db	1280	CCTCGATAAGAGAAATGTCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTAGAGGA	1339
Qy	1021	GGGTGAGATTAAGAGACCTTTTCTACCAAGCAACCAACTTACTACTAGCTGCAATGCA	1080
Db	1340	GGGTGAGATTAAGAGACCTTTTCTACCAAGCAACCAACTTACTACTAGCTGCAATGCA	1399
Qy	1081	ATGAACCAACAGTGGTGTGCTGAGTCTCAGCCCTTGTCTTAAATGCCATGGCAAGTAGAAA	1140
Db	1400	ATGAACCAACAGTGGTGTGCTGAGTCTCAGCCCTTGTCTTAAATGCCATGGCAAGTAGAAA	1459
Qy	1141	GGTATATCATCAACTTCTATACCTAAAGAAATATAGGATTTGCAATTAATAATAGTTTGG	1200
Db	1460	GGTATATCATCAACTTCTATACCTAAAGAAATATAGGATTTGCAATTAATAATAGTTTGG	1519
Qy	1201	GTTATATATGCAACAAACACACACAGAAATATATTCATGCTCTATGTTATATAGATCAAT	1260
Db	1520	GTTATATATGCAACAAACACACACAGAAATATATTCATGCTCTATGTTATATAGATCAAT	1579
Qy	1261	GTTTTTTTGGTATATATAACCGGTACACACAGAGCTTACATATGTTTGGTGGTAGACTCT	1320
Db	1580	GTTTTTTTGGTATATATAACCGGTACACACAGAGCTTACATATGTTTGGTGGTAGACTCT	1639
Qy	1321	TAAATCCTTTGCCAAATTAAGGGATGTTCAAAATATATGAAACATGCTTTTGAAGAAATTT	1380
Db	1640	TAAATCCTTTGCCAAATTAAGGGATGTTCAAAATATATGAAACATGCTTTTGAAGAAATTT	1699
Qy	1381	AGGAGATAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT	1440
Db	1700	AGGAGATAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT	1759
Qy	1441	AAGAAAGCATCTCTATATTAATAAATCAAAAGATGAGGCTTCTTACATATACATCTTAG	1500
Db	1760	AAGAAAGCATCTCTATATTAATAAATCAAAAGATGAGGCTTCTTACATATACATCTTAG	1819
Qy	1501	TTGATTATTAAAAAGGAAAAAGGTTTCCAGAGAAAAAGGCAATACCTTAAGCATTTTTC	1560
Db	1820	TTGATTATTAAAAAGGAAAAAGGTTTCCAGAGAAAAAGGCAATACCTTAAGCATTTTTC	1879
Qy	1561	CATGAGAGCATGCTGATCTTACCTATGAGCTGTAATAACCTGCTCTCCTCAAAACCATGTC	1620
Db	1880	CATGAGAGCATGCTGATCTTACCTATGAGCTGTAATAACCTGCTCTCCTCAAAACCATGTC	1939
Qy	1621	CATATAATATAAGTCTTTAGAAATTAATAATTTTATGCTTTTATGCAATTTTGTGAGG	1680
Db	1940	CATATAATATAAGTCTTTAGAAATTAATAATTTTATGCTTTTATGCAATTTTGTGAGG	1999
Qy	1681	CATCTTATTATTAATTAACCTCTCTCAAAACCTTACTTTAGAGGTTTTTTTATATAGTCT	1740
Db	2000	CATCTTATTATTAATTAACCTCTCTCAAAACCTTACTTTAGAGGTTTTTTTATATAGTCT	2059
Qy	1741	CTACAAAAAGACAATGATTAAGCTGTAAACAGAAATTTTGAATTTTGTCTTTTGCACAAACC	1800
Db	2060	CTACAAAAAGACAATGATTAAGCTGTAAACAGAAATTTTGAATTTTGTCTTTTGCACAAACC	2119
Qy	1801	CTCCACAAAGCAATCCCTTTCAAGAAATGGCATCTCTGTATGAACTTTTCCAGAT	1860
Db	2120	CTCCACAAAGCAATCCCTTTCAAGAAATGGCATCTCTGTATGAACTTTTCCAGAT	2179

RESULT 4

US-09-540-224-1

; Sequence 1, Application US/09540224

; Patent No. 6468543

; GENERAL INFORMATION:

; APPLICANT: Gilbertson, Debra G.

; APPLICANT: Hart, Charles E.

; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,

; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4

; FILE REFERENCE: 00-28

; CURRENT APPLICATION NUMBER: US/09/540,224

; CURRENT FILING DATE: 2000-03-31

; EARLIER APPLICATION NUMBER: US 60/180,169

; EARLIER FILING DATE: 2000-02-04

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 1882

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (226)...(1338)

US-09-540-224-1

Query Match 77.1%; Score 1491.8; DB 4; Length 1882;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 1507; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

QY	1	TTGTACCAAGAGATGACGACATCCAGGTGAAGGAAACGGCTAGCTCAGAGTCTTAGA	60
DB	370	TTGTACCAAGAGATGACGACATCCAGGTGAAGGAAACGGCTAGCTCAGAGTCTTAGA	429
QY	61	TTCCGGAACAGCTACCCAGGAACTCTCTGACATGCGCGCTTCACTCTCAGAGAAAT	120
DB	430	TTCCGGAACAGCTACCCAGGAACTCTCTGACATGCGCGCTTCACTCTCAGAGAAAT	489
QY	121	ACACGGATACAGTGTGTTGACAAATCAGTTTGGATTAGAGGAAAGCAAAATGATATC	180
DB	490	ACACGGATACAGTGTGTTGACAAATCAGTTTGGATTAGAGGAAAGCAAAATGATATC	549
QY	181	TGTAGGTATGATTTTGTGGAGTTGAAGATATATCCGAAACAGTACCATTATTAGAGA	240
DB	550	TGTAGGTATGATTTTGTGGAGTTGAAGATATATCCGAAACAGTACCATTATTAGAGA	609
QY	241	CGATCGTGTGGACACAAAGGAGTTCCTCCAGGATAAAATCAAGAACGAAACCAAAATTA	300
DB	610	CGATCGTGTGGACACAAAGGAGTTCCTCCAGGATAAAATCAAGAACGAAACCAAAATTA	669
QY	301	ATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTATTATTCT	360
DB	670	ATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTATTATTCT	729
QY	361	TTGCTGGAAAGATTTCCAAACCCAGCAGCTTCAGAGACCACTGGGAATCTGTCAAGC	420
DB	730	TTGCTGGAAAGATTTCCAAACCCAGCAGCTTCAGAGACCACTGGGAATCTGTCAAGC	789
QY	421	TCTATTTCAGGGGTATCCTATAACTCTCCATCAGTAAACGATCCCACTGTGATCGGAT	480
DB	790	TCTATTTCAGGGGTATCCTATAACTCTCCATCAGTAAACGATCCCACTGTGATCGGAT	849
QY	481	GCTCTGGACAAAAAATTTGAGAAATTTGATACAGTGGGAAGATCTGCTCAAGTACTTCAAT	540
DB	850	GCTCTGGACAAAAAATTTGAGAAATTTGATACAGTGGGAAGATCTGCTCAAGTACTTCAAT	909
QY	541	CCAGAGTCTATGGCAAGAGATCTTGAGAAATTTGATCTGGACACCCCTCGGTATCGAGC	600
DB	910	CCAGAGTCTATGGCAAGAGATCTTGAGAAATTTGATCTGGACACCCCTCGGTATCGAGC	969
QY	601	AGTCTATACCATCACCAGGAGTCAGAAATTTGACCTGATAGGCTCAATGATGATGCAAG	660
DB	970	AGTCTATACCATCACCAGGAGTCAGAAATTTGACCTGATAGGCTCAATGATGATGCAAG	1029

QY	661	CGTTACAGTTGCACTCCAGGAATTTACTCGGTCAATATAAGAGAAAGAGCTGAAGTTGGCC	720
DB	1030	CGTTACAGTTGCACTCCAGGAATTTACTCGGTCAATATAAGAGAAAGAGCTGAAGTTGGCC	1089
QY	721	AATGTGCTCTTTTCCACGTTGCTCTCTCGTCAGCGCTGTGAGGAAATTTGGTGT	780
DB	1090	AATGTGCTCTTTTCCACGTTGCTCTCTCGTCAGCGCTGTGAGGAAATTTGGTGT	1149
QY	781	GGAATCTCACTGGAGGCTCTGCACATGCAATTCAGGAAACCGTGAAGATATCAT	840
DB	1150	GGAATCTCACTGGAGGCTCTGCACATGCAATTCAGGAAACCGTGAAGATATCAT	1209
QY	841	GAGTATTTACAGTTTGGAGCTTGGCCACATCAAGAGAGGGGTAGAGCTTAAGACCATGCT	900
DB	1210	GAGTATTTACAGTTTGGAGCTTGGCCACATCAAGAGAGGGGTAGAGCTTAAGACCATGCT	1269
QY	901	CTAGTTGACATCCAGTTGGATCACCATGAAGGATGCGATTGTATCTGCAGCTCAAGACCA	960
DB	1270	CTAGTTGACATCCAGTTGGATCACCATGAAGGATGCGATTGTATCTGCAGCTCAAGACCA	1329
QY	961	CTCGATAAGAGAAATGTGCACATCCTTTACATTAAGCTTGAAGAAACCTTTAGTTAAGGA	1020
DB	1330	CTCGATAAGAGAAATGTGCACATCCTTTACATTAAGCTTGAAGAAACCTTTAGTTAAGGA	1389
QY	1021	GGGTGAGATAAGAGACCCCTTTTCTTACAGCAACCAAACTTACTAGCTGCAATGCA	1080
DB	1390	GGGTGAGATAAGAGACCCCTTTTCTTACAGCAACCAAACTTACTAGCTGCAATGCA	1449
QY	1081	ATGAACACAAAGTGTGCTGAGTCTCAGCCTTGTCTTTTAAATGCCATGGCAAGTAGAAA	1140
DB	1450	ATGAACACAAAGTGTGCTGAGTCTCAGCCTTGTCTTTTAAATGCCATGGCAAGTAGAAA	1509
QY	1141	GGTATATCATCAACTTCTATACCTTAAGAAATAGGATTTGCAATTAATAGTGTTCAG	1200
DB	1510	GGTATATCATCAACTTCTATACCTTAAGAAATAGGATTTGCAATTAATAGTGTTCAG	1569
QY	1201	GTTATATATGCACAAACACACACAGAAATATATTATCATGCTCTATGTATATAGATCAAT	1260
DB	1570	GTTATATATGCACAAACACACACAGAAATATATTATCATGCTCTATGTATATAGATCAAT	1629
QY	1261	G-----TTTTTTTGGTATATATAACAGGTACACAGAGCTTACATATGTTTGAAGTTAGA	1316
DB	1630	GTTTTTTTTTTTGGTATATATAACAGGTACACAGAGGTACATATGTTTGAAGTTAGA	1689
QY	1317	CTCTTAAATCCTTTGCCAAATTAAGGATGGTCAATATATATGAAACATGCTTTTAGAAA	1376
DB	1690	CTCTTAAATCCTTTGCCAAATTAAGGATGGTCAATATATATGAAACATGCTTTTAGAAA	1749
QY	1377	ATTTAGGAGATAAATTTTAAATTTTAAATTTTAAACACAAACAAATTTTGAATCTTGCTCT	1436
DB	1750	ATTTAGGAGATAAATTTTAAATTTTAAATTTTAAATTTTAAACACAAACAAATTTTGAATCTTGCTCT	1809
QY	1437	CTTAAAGAAAGCATCTTGTATATTAAATTAATAAATCAAAAGATGAGGCTTTCTTACATATACATC	1496
DB	1810	CTTAAAGAAAGCATCTTGTATATTAAATTAATAAATCAAAAGATGAGGCTTTCTTACATATACATC	1869
QY	1497	TTAGTTGATTATT 1509	
DB	1870	TTAGTTGATTATT 1882	

RESULT 5

US-09-564-595D-1

; Sequence 1, Application US/09564595D

; Patent No. 6495668

; GENERAL INFORMATION:

; APPLICANT: Gilbert, Teresa

; APPLICANT: Hart, Charles E.

; APPLICANT: Sheppard, Paul O.

; TITLE OF INVENTION: GROWTH FACTOR HOMOLOGY ZVEGF4

; FILE REFERENCE: 99-19

; CURRENT APPLICATION NUMBER: US/09/564,595D

; CURRENT FILING DATE: 2000-05-03

PRIOR APPLICATION NUMBER: US 09/304,216
PRIOR FILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1882
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (226)...(1338)
US-09-564-595D-1

Query Match 77.1%; Score 1491.8; DB 4; Length 1882;
Best Local Similarity 99.6%; Pred. No. 0;

Matches 1507; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

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QY 1 TTGTACCGAAGATGAGACCTCCAGGTCAAGGAACGGCTACGTGAGAGTCTCTAGA 60
Db 370 TTGTACCGAAGATGAGACCTCCAGGTCAAGGAACGGCTACGTGAGAGTCTCTAGA 429
QY 61 TTCCCGAAGACGCTACCCAGGAACCTGCTCCGACATGGCGGCTTCACTCTCAGGAGAT 120
Db 430 TTCCCGAAGACGCTACCCAGGAACCTGCTCCGACATGGCGGCTTCACTCTCAGGAGAT 489
QY 121 ACAGGATACAGTAGTGTGTTGACAACTAGTTGGATTAGAGAAAGACGAAATGATATC 180
Db 490 ACAGGATACAGTAGTGTGTTGACAACTAGTTGGATTAGAGAAAGACGAAATGATATC 549
QY 181 TGTAGTATGATTTTGTGGAAGTTGAAGATATATCCGAACCGAGTACATTAATAGAGGA 240
Db 550 TGTAGTATGATTTTGTGGAAGTTGAAGATATATCCGAACCGAGTACATTAATAGAGGA 609
QY 241 CGATGTTGTGGACACAAAGGAAGTTCTCCAGGATAAATCAAGAACGAAACCAAAATTTAA 300
Db 610 CGATGTTGTGGACACAAAGGAAGTTCTCCAGGATAAATCAAGAACGAAACCAAAATTTAA 669
QY 301 ATCAGATTCAAGTCGATGACTACTTTGGTAAACCTGGATTCAAGATTATTTCT 360
Db 670 ATCAGATTCAAGTCGATGACTACTTTGGTAAACCTGGATTCAAGATTATTTCT 729
QY 361 TTGCTGGAAGATTTCCAAACCGCAGAGCTTCAGAGACCAACTGGGAATCTGTCAAGC 420
Db 730 TTGCTGGAAGATTTCCAAACCGCAGAGCTTCAGAGACCAACTGGGAATCTGTCAAGC 789
QY 421 TCTATTTCAGGGGTATFCTTAACTCTCCATCAGTAAACGGATCCCACTCTGATTGGGAT 480
Db 790 TCTATTTCAGGGGTATFCTTAACTCTCCATCAGTAAACGGATCCCACTCTGATTGGGAT 849
QY 481 GCTCTGGACAAAAAATTCAGAAATTTGATACAGTGGAAAGATCTGCTCAAGTCTCAAT 540
Db 850 GCTCTGGACAAAAAATTCAGAAATTTGATACAGTGGAAAGATCTGCTCAAGTCTCAAT 909
QY 541 CCAGAGTCATGCAAGAGATCTTGAGAAATGATCTCGACACCCCTCGGTATCGAGC 600
Db 910 CCAGAGTCATGCAAGAGATCTTGAGAAATGATCTCGACACCCCTCGGTATCGAGC 969
QY 601 AGGTCAATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
Db 970 AGGTCAATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 1029
QY 661 CGTTACAGTTGACCTCCAGGAATTTACTCGGTCAATATAGAGAGAGCTGAAGTTGGC 720
Db 1030 CGTTACAGTTGACCTCCAGGAATTTACTCGGTCAATATAGAGAGAGCTGAAGTTGGC 1089
QY 721 AATGTGGTCTTTTCCAGCTTGCCTCCCTGCGAGCGCTGTGGAGGAATTTGTGGCTGT 780
Db 1090 AATGTGGTCTTTTCCAGCTTGCCTCCCTGCGAGCGCTGTGGAGGAATTTGTGGCTGT 1149
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QY 781 GGAACTGTCAACTGGAGGTCTCTGCACATGCAATTCAGGAAAAACCGTGAAGATATCAT 840
Db 1150 GGAACTGTCAACTGGAGGTCTCTGCACATGCAATTCAGGAAAAACCGTGAAGATATCAT 1209
QY 841 GAGGTATTACAGTTTGGAGCTGGCCACATCAAGAGAGGGGTAGAGCTTAAGACCATGCT 900
Db 1210 GAGGTATTACAGTTTGGAGCTGGCCACATCAAGAGAGGGGTAGAGCTTAAGACCATGCT 1269
QY 901 CTAGTTGACATCCAGTTCGATCACCATGAACGATGCGATTGTATCTGAGCTCAAGACA 960
Db 1270 CTAGTTGACATCCAGTTCGATCACCATGAACGATGCGATTGTATCTGAGCTCAAGACA 1329
QY 961 CCTCGATAAGAGAAATGTGCACATCCTTACATTAAGCTTGAAGAACCTTTAGTTTAAAGA 1020
Db 1330 CCTCGATAAGAGAAATGTGCACATCCTTACATTAAGCTTGAAGAACCTTTAGTTTAAAGA 1389
QY 1021 GGGTCAGATAAGAGAACCTTTTCTTACCCAGCAACAAACTTACTAGCTTGCATATGCA 1080
Db 1390 GGGTCAGATAAGAGAACCTTTTCTTACCCAGCAACAAACTTACTAGCTTGCATATGCA 1449
QY 1081 ATGAACACAAAGTGGTGGTGGTCTGAGTCTCAGCCTTGTCTTAAATGCAATGCAAGTAA 1140
Db 1450 ATGAACACAAAGTGGTGGTGGTCTGAGTCTCAGCCTTGTCTTAAATGCAATGCAAGTAA 1509
QY 1141 GGTATATCATCAACTTCTATACCTTAAGAAATATAGGATTGCAATTAATATAGTGTTCAG 1200
Db 1510 GGTATATCATCAACTTCTATACCTTAAGAAATATAGGATTGCAATTAATATAGTGTTCAG 1569
QY 1201 GTTATATATGACAAACACACACAGAAATATATTCATGCTATGTGTATATAGATCAAT 1260
Db 1570 GTTATATATGACAAACACACAGAAATATATTCATGCTATGTGTATATAGATCAAT 1629
QY 1261 G-----TTTTTTTGTGATATATATACCGGTACACAGAGCTTACATATGTTGAGTTAGA 1316
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QY 1317 CTCTTAAATCCTTTGGCCAAATTAAGGATGGTCAATATATATGAACATGTCTTTAGAAA 1376
Db 1690 CTCTTAAATCCTTTGGCCAAATTAAGGATGGTCAATATATATGAACATGTCTTTAGAAA 1749
QY 1377 ATTTAGGAGATAAATTTATTTTAAATTTTGAACACAAAAATTTGAATCTTGCTCT 1436
Db 1750 ATTTAGGAGATAAATTTATTTTAAATTTTGAACACAAAAATTTGAATCTTGCTCT 1809
QY 1437 CTTAAAGAAAGCATCTTGATATATTAATAATCAAAAGATGAGGCTTTCTTACATATACATC 1496
Db 1810 CTTAAAGAAAGCATCTTGATATATTAATAATCAAAAGATGAGGCTTTCTTACATATACATC 1869
QY 1497 TTAGTTGATTATT 1509
Db 1870 TTAGTTGATTATT 1882
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RESULT 6

US-09-706-968-36
; Sequence 36, Application US/09706968
; Patent No. 6528050
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOGY ZVEGF3
; FILE REFERENCE: 98-60C1
; CURRENT APPLICATION NUMBER: US/09/706,968
; CURRENT FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: US/09/541,752
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0

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; SEQ ID NO 36
; LENGTH: 1882
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (226)...(1338)
US-09-706-968-36

Query Match      77.1%; Score 1491.8; DB 4; Length 1882;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1507; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

Qy 1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAGAAACGGCTACGTGCAGAGTCCTAGA 60
Db 370 TTGTACCGAAGAGATGAGACCATCCAGGTGAAGAAACGGCTACGTGCAGAGTCCTAGA 429

Qy 61 TTCCCGACAGCTACCCAGCAACCTCTCTCTGACATGCGCGCTTCACTCTCAGGAGAT 120
Db 430 TTCCCGACAGCTACCCAGCAACCTCTCTCTGACATGCGCGCTTCACTCTCAGGAGAT 489

Qy 121 ACAGGATACAGTAGTGTGTTGCAATCAGTGTGATTTAGAGGAAGCAGAAAATGATATC 180
Db 490 ACAGGATACAGTAGTGTGTTGCAATCAGTGTGATTTAGAGGAAGCAGAAAATGATATC 549

Qy 181 TGTAGGTATGATTTGTGGAAAGTTGAAGATATATCCGAAACAGTACCATTTATAGAGGA 240
Db 550 TGTAGGTATGATTTGTGGAAAGTTGAAGATATATCCGAAACAGTACCATTTATAGAGGA 609

Qy 241 CGATGGTGTGACACCAAGGAAGTTCTCCCAAGGATAAATCAAGAACCAATTTAAA 300
Db 610 CGATGGTGTGACACCAAGGAAGTTCTCCCAAGGATAAATCAAGAACCAATTTAAA 669

Qy 301 ATCATTCAAGTCGATGACTTCTTGTGCTAAACCTGATTTCAAGATTTATTTCT 360
Db 670 ATCATTCAAGTCGATGACTTCTTGTGCTAAACCTGATTTCAAGATTTATTTCT 729

Qy 361 TTGCTGGAAGATTTCCAAACCCGACGAGCTTTAGAGACCAATCGGAAATCTGTCAAGC 420
Db 730 TTGCTGGAAGATTTCCAAACCCGACGAGCTTTAGAGACCAATCGGAAATCTGTCAAGC 789

Qy 421 TCTATTTTCAGGGGTATCTATACTCTCATCAGTAAAGGATCCCACTCTGATTCGGAT 480
Db 790 TCTATTTTCAGGGGTATCTATACTCTCATCAGTAAAGGATCCCACTCTGATTCGGAT 849

Qy 481 GCTCTGGAACAAAATTTGCAGAAATTTGATACAGTGAAGATCTGCTCAAGTACTTCAAT 540
Db 850 GCTCTGGAACAAAATTTGCAGAAATTTGATACAGTGAAGATCTGCTCAAGTACTTCAAT 909

Qy 541 CCAGAGTCATGCGCAAGAAAGATCTTGAGAAATATGATCTGGACACCCCTCGGTATCGAGGC 600
Db 910 CCAGAGTCATGCGCAAGAAAGATCTTGAGAAATATGATCTGGACACCCCTCGGTATCGAGGC 969

Qy 601 AGGTATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
Db 970 AGGTATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 1029

Qy 661 CGTTACAGTTCACCTCCAGGAATTTACTCGGTCAATATAAGAGAGAGCTCAAGTTGGCTGT 720
Db 1030 CGTTACAGTTCACCTCCAGGAATTTACTCGGTCAATATAAGAGAGAGCTCAAGTTGGCTGT 1089

Qy 721 AATGTGCTTCTTTTCCACGTTGCTCTCTGTCAGCGCTCTGAGGAGAAATTTGGCTGT 780
Db 1090 AATGTGCTTCTTTTCCACGTTGCTCTCTGTCAGCGCTCTGAGGAGAAATTTGGCTGT 1149

Qy 781 GGAATGTCAACTGAGGTCTGCAATGCAATTCAGGGAACCGTGAAGAAAGTATCAT 840
Db 1150 GGAATGTCAACTGAGGTCTGCAATGCAATTCAGGGAACCGTGAAGAAAGTATCAT 1209

Qy 841 GAGGTATTACAGTTTGAAGCTGGCCACATCAAGAGGGGTAGAGCTTAAGACCATGGCT 900
Db 1210 GAGGTATTACAGTTTGAAGCTGGCCACATCAAGAGGGGTAGAGCTTAAGACCATGGCT 1269
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Qy 901 CTAGTTCACATCCAGTTGGATCACCATGAACGATGCGATTGCTATCTGCAGCTCAAGACCA 960
Db 1270 CTAGTTCACATCCAGTTGGATCACCATGAACGATGCGATTGCTATCTGCAGCTCAAGACCA 1329

Qy 961 CCTCGATAAGAGAAATGTGCATCTTTACATTTAAGCCTGAAAGAAACCTTTAGTTTAAGGA 1020
Db 1330 CCTCGATAAGAGAAATGTGCATCTTTACATTTAAGCCTGAAAGAAACCTTTAGTTTAAGGA 1389

Qy 1021 GGGTGAGATAAGAGACCCCTTTTCTACAGCAACCAAACTTACTAGCTGCAATGCA 1080
Db 1390 GGGTGAGATAAGAGACCCCTTTTCTACAGCAACCAAACTTACTAGCTGCAATGCA 1449

Qy 1081 ATGNAACAAGTGGTCTGAGTCTCAGCTTGTGTTGTTAATGCCAATGCAAGTAGAAA 1140
Db 1450 ATGNAACAAGTGGTCTGAGTCTCAGCTTGTGTTGTTAATGCCAATGCAAGTAGAAA 1509

Qy 1141 GGTATATCATCAACTTCTATACCTTAAGATATAGGATTTGCAATTAATAATAGTTTGGAG 1200
Db 1510 GGTATATCATCAACTTCTATACCTTAAGATATAGGATTTGCAATTAATAATAGTTTGGAG 1569

Qy 1201 GTTATATATGCACAAACACACACAGAAATATATTTCTATCTATGTATATAGATCAAT 1260
Db 1570 GTTATATATGCACAAACACACACAGAAATATATTTCTATCTATGTATATAGATCAAT 1629

Qy 1261 G-----TTTTTTTGGTATATATACAGGTTACACAGAGCTTACATATGTTGAGTTAGA 1316
Db 1630 GTTTTTTTTTTTTTGGTATATATACAGGTTACACAGAGCTTACATATGTTGAGTTAGA 1689

Qy 1317 CTCTTAAATACCTTTGCAAAATTAAGGATGTCAAATATATAGAAACATGCTTTTAGAAA 1376
Db 1690 CTCTTAAATACCTTTGCAAAATTAAGGATGTCAAATATATAGAAACATGCTTTTAGAAA 1749

Qy 1377 ATTTAGGAGATAAATTTTAAATTTTGAACACACAAAACAAATTTTGAATCTTGTCTCT 1436
Db 1750 ATTTAGGAGATAAATTTTAAATTTTGAACACACAAAACAAATTTTGAATCTTGTCTCT 1809

Qy 1437 CTTAAAGAAAGCATCTTGTATATTTAAATAACAAAGATGAGGCTTCTTACATATACATC 1496
Db 1810 CTTAAAGAAAGCATCTTGTATATTTAAATAACAAAGATGAGGCTTCTTACATATACATC 1869

Qy 1497 TTAGTTGATTAAT 1509
Db 1870 TTAGTTGATTAAT 1882

RESULT 7
US-09-808-972-1
; Sequence 1, Application US/09808972
; Patent No. 6630142
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 00-79
; CURRENT APPLICATION NUMBER: US/09/808,972
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/235,295
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/132,250
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1882
; TYPE: DNA
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (226)....(1338)
US-09-808-972-1

Query Match 77.1%; Score 1491.8; DB 4; Length 1882;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1507; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

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QY 1 TTGTACCGAGAGATGAGACCACTCAGGTGAAGGAAACGGCTAGCTGCAGAGTCTCTAGA 60
DB 370 TTGTACCGAGAGATGAGACCACTCAGGTGAAGGAAACGGCTAGCTGCAGAGTCTCTAGA 429
QY 61 TTCCCGAACAGCTACCCACGAGAACCTGCTCCTCGACATCGCGGCTTCACTCTCAGGAGAT 120
DB 430 TTCCCGAACAGCTACCCACGAGAACCTGCTCCTCGACATCGCGGCTTCACTCTCAGGAGAT 489
QY 121 ACACGGATACAGCTAGTGTGTTGCAATCAGTTTGGATTAGAGGAAAGCAAAATGATATC 180
DB 490 ACACGGATACAGCTAGTGTGTTGCAATCAGTTTGGATTAGAGGAAAGCAAAATGATATC 549
QY 181 TGTAGGTATGATTTTGTGGAAGTTGAAGTATATCCGAAACAGTACCAATTATTAGAGGA 240
DB 550 TGTAGGTATGATTTTGTGGAAGTTGAAGTATATCCGAAACAGTACCAATTATTAGAGGA 609
QY 241 CCATGGTGGGACACAAAGGAAGTCTCCCAAGGATAAAATCAAGAACGAAACCAAAATTTAA 300
DB 610 CGATGGTGGGACACAAAGGAAGTCTCCCAAGGATAAAATCAAGAACGAAACCAAAATTTAA 669
QY 301 ATCAATTCAAGTCCGATGACTACTTTGGCTAAACCTGGATTCAAGATTATTATTCT 360
DB 670 ATCAATTCAAGTCCGATGACTACTTTGGCTAAACCTGGATTCAAGATTATTATTCT 729
QY 361 TTGCTGGAGATTTCCAAACCCGACAGCTTCAGAGACCAACTGGAACTGTCTCAGACG 420
DB 730 TTGCTGGAGATTTCCAAACCCGACAGCTTCAGAGACCAACTGGAACTGTCTCAGACG 789
QY 421 TCTATTTTCAAGGGTATCTTAACTCTCCATCAGTAAACGGATCCCACTCTGATTCGGAT 480
DB 790 TCTATTTTCAAGGGTATCTTAACTCTCCATCAGTAAACGGATCCCACTCTGATTCGGAT 849
QY 481 GCTCTGGACAAAAATTTGAGAAATTTGATACAGTGGAGATCTGCTCAAGTACTTCAAT 540
DB 850 GCTCTGGACAAAAATTTGAGAAATTTGATACAGTGGAGATCTGCTCAAGTACTTCAAT 909
QY 541 CCAGATCATGCGACAGAGATCTTGAGATATGATCTGACACCCCTCGGTATCGAGGC 600
DB 910 CCAGATCATGCGACAGAGATCTTGAGATATGATCTGACACCCCTCGGTATCGAGGC 969
QY 601 AGGTCTATCATGACCGGAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
DB 970 AGGTCTATCATGACCGGAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 1029
QY 661 CGTTACAGTTGCACTCCCAAGGAATTTCTCGTCAATATAAGAGAGAGCTGAAGTTGGCC 720
DB 1030 CGTTACAGTTGCACTCCCAAGGAATTTCTCGTCAATATAAGAGAGAGCTGAAGTTGGCC 1089
QY 721 AATGTGGTCTTTTCCAGGTTGCTCTCGTGGAGCGCTGTGGAGAAATTTGTGGCTGT 780
DB 1090 AATGTGGTCTTTTCCAGGTTGCTCTCGTGGAGCGCTGTGGAGAAATTTGTGGCTGT 1149
QY 781 GGAACTGTCAACTGGAGGTCCTGCAATGCAATTCAGGGAACCGTGAAGGATATCAT 840
DB 1150 GGAACTGTCAACTGGAGGTCCTGCAATGCAATTCAGGGAACCGTGAAGGATATCAT 1209
QY 841 GAGGTATTACAGTTTGAAGCTTGGCCACATCAAGAGAGGGGTAGAGCTAAGACCATGGCT 900
DB 1210 GAGGTATTACAGTTTGAAGCTTGGCCACATCAAGAGAGGGGTAGAGCTAAGACCATGGCT 1269
QY 901 CTAGTTGATCATCCAGTTGATCAGTACCATGAGGATTTGATCTGCGAGCTCAGAGCA 960
DB 1270 CTAGTTGATCATCCAGTTGATCAGTACCATGAGGATTTGATCTGCGAGCTCAGAGCA 1329
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RESULT 8

US-10-140-002-185
; Sequence 185, Application US/10140002
; Patent No. 6725730

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC59
; CURRENT APPLICATION NUMBER: US/10/140,002
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 185
; LENGTH: 1162

; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-002-185

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Query Match      51.9%; Score 1003.4; DB 4; Length 1162;
Best Local Similarity 99.9%; Pred. No. 1.1e-253;
Matches 1004; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGAAACGGCTACGTCCAGAGTCTTAGA 60
Db 158 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGAAACGGCTACGTCCAGAGTCTTAGA 217
Qy 61 TTCCGACAGCTACCCAGGAACTCTCTGACATCGCGCTTCACTCTCAGAGAT 120
Db 218 TTCCGACAGCTACCCAGGAACTCTCTGACATCGCGCTTCACTCTCAGAGAT 277
Qy 121 ACACGGATACAGTGTGTTGACAACTCAGTTTGGATTAGAGGAAAGCAAGAAATGATATC 180
Db 278 ACACGGATACAGTGTGTTGACAACTCAGTTTGGATTAGAGGAAAGCAAGAAATGATATC 337
Qy 181 TGTAGTATGATTTTGTGGAAAGTTGAAGATATATCCGAAACAGTACCATATTAGAGGA 240
Db 338 TGTAGTATGATTTTGTGGAAAGTTGAAGATATATCCGAAACAGTACCATATTAGAGGA 397
Qy 241 CGATGGTGTGGACACAGGAAGTCTCTCAAGGATAAATCAAGAACCAACCAATTTAA 300
Db 398 CGATGGTGTGGACACAGGAAGTCTCTCAAGGATAAATCAAGAACCAACCAATTTAA 457
Qy 301 ATCATTCAAGTCGAGTACTTCTGCTAACTGCTGCTAACTGCTGCTAACTGCTGCT 360
Db 458 ATCATTCAAGTCGAGTACTTCTGCTAACTGCTGCTAACTGCTGCTGCTGCTGCT 517
Qy 361 TTGCTGGAAGATTTCCAAACCGCAGCAGCTTCAGAGACCAACTGGGAATCTGTCAACAGC 420
Db 518 TTGCTGGAAGATTTCCAAACCGCAGCAGCTTCAGAGACCAACTGGGAATCTGTCAACAGC 577
Qy 421 TCTATTTTCAGGGTATCTTAATCTCTCACTGATTAACGGATCCCACTGATTCGGAT 480
Db 578 TCTATTTTCAGGGTATCTTAATCTCTCACTGATTAACGGATCCCACTGATTCGGAT 637
Qy 481 GCTCTGGACAAATAATTTGCAAGATTTGATACAGTGGAAAGATCTGCTCAAGTACTTCAAT 540
Db 638 GCTCTGGACAAATAATTTGCAAGATTTGATACAGTGGAAAGATCTGCTCAAGTACTTCAAT 697
Qy 541 CCAGAGTCATGCGAAGAGATCTTGAGAAATGTATCTGGACACCCCTCGGTATCGAGGC 600
Db 698 CCAGAGTCATGCGAAGAGATCTTGAGAAATGTATCTGGACACCCCTCGGTATCGAGGC 757
Qy 601 AGGTATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
Db 758 AGGTATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 817
Qy 661 CGTTACAGTTGACCTCCAGGAATTTACTCGGTCAATATAAGAGAGAGCTGAAGTTGGCC 720
Db 818 CGTTACAGTTGACCTCCAGGAATTTACTCGGTCAATATAAGAGAGAGCTGAAGTTGGCC 877
Qy 721 AATGTGCTCTTCTTTCCAGCTTGCCTCTCGTGGACAGCCTGTGGAGGAAATTTGTGGCTGT 780
Db 878 AATGTGCTCTTCTTTCCAGCTTGCCTCTCGTGGACAGCCTGTGGAGGAAATTTGTGGCTGT 937
Qy 781 GGAATGTCAACTGAGGTCTGCAATGCAATTCAGGAAACCGTGAAGAAATGATATCAT 840
Db 938 GGAATGTCAACTGAGGTCTGCAATGCAATTCAGGAAACCGTGAAGAAATGATATCAT 997
Qy 841 GAGGTATTTACAGTTTGGCTGGCCACATCAAGAGAGGGGTAGAGCTTAAGACCATGGCT 900
Db 998 GAGGTATTTACAGTTTGGCTGGCCACATCAAGAGAGGGGTAGAGCTTAAGACCATGGCT 1057
Qy 901 CTAGTTGACATCCAGTTGGATCAACCATGAACGATCGGATTTGTATCTGCAAGCTCAAGACCA 960
Db 1058 CTAGTTGACATCCAGTTGGATCAACCATGAACGATCGGATTTGTATCTGCAAGCTCAAGACCA 1117
Qy 961 CCTCGATAAGAGATGTGCAATCTTTACATTAAGCCTGAAAGAA 1005
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Db 1118 CCTCGATAAGAGATGTGCAATCTTACATTAAAGCCTGAGAGAA 1162

RESULT 9
US-09-540-224-3
; Sequence 3, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540.224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180.169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (93)...(1205)
US-09-540-224-3
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Query Match 41.1%; Score 795.4; DB 4; Length 1472;
Best Local Similarity 78.7%; Pred. No. 5.1e-199;
Matches 1007; Conservative 0; Mismatches 226; Indels 46; Gaps 3;

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Qy 1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGAAACGGCTACGTCCAGAGTCTTAGA 60
Db 237 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGAAACGGCTACGTCCAGAGTCTTAGA 296
Qy 61 TTCCGAAACAGCTACCCAGGAACTCTCTCTGACATCGCGCTTCACTCTCAGAGAT 120
Db 297 TTCCGAAACAGCTACCCAGGAACTCTCTCTGACATCGCGCTTCACTCTCAGAGAT 356
Qy 121 ACAGGATACAGTGTGTTGCAATCAGTTTGGATTAGAGGAAAGCAAGAAATGATATC 180
Db 357 ACAGGATACAGTGTGTTGCAATCAGTTTGGATTAGAGGAAAGCAAGAAATGATATC 416
Qy 181 TGTAGTATGATTTTGTGGAAAGTTGAAGATATATCCGAAACAGTACCATATTAGAGGA 240
Db 417 TGTAGTATGATTTTGTGGAAAGTTGAAGATATATCCGAAACAGTACCATATTAGAGGA 476
Qy 241 CGATGGTGTGGACACAAAGGAAGTTCTCTCAAGGATAAATCAAGAAACCAAAATTTAA 300
Db 477 AGATGGTGTGGCCACAAGGAGATCCCTCAAGGATAAATCAAGAAACCAAAATTTAA 536
Qy 301 ATCATTCAAGTCCGATGACTTCTGTGGCTAAACCTGGATTCAAGATTTATTTCT 360
Db 537 ATCATTCAAGTCCGATGACTTCTGTGGCTAAACCTGGATTCAAGATTTATTTCTCA 596
Qy 361 TTGCTGGAAGATTTTCCAAACCGCAGCAGCTTCAGAGACCAACTGGGAATCTGTCAAGC 420
Db 597 TTTGTTGGAAGATTTTCCAAACCGCAGCAGCTTCAGAGACCAACTGGGAATCTGTCAAGC 656
Qy 421 TCTATTTTCAGGGTATCTTAACTTCTTCAATCACTGATTAACGGATCCCACTCTGATTCGGAT 480
Db 657 TCTATTTTCAGGGTATCTTAACTTCTTCAATCACTGATTAACGGATCCCACTCTGATTCGGAT 716
Qy 481 GCTCTGGACAAATAATTTGCAAGATTTGATACAGTGGAAAGATCTGCTCAAGTACTTCAAT 540
Db 717 GCTCTGGACAAATAATTTGCAAGATTTGATACAGTGGAAAGATCTGCTCAAGTACTTCAAT 776
Qy 541 CCAGAGTCATGCGAAGAGATCTTTGAGAAATGTATCTGGACACCCCTCGGTATCGAGGC 600
Db 777 CCAGTCCTTGGCAAGATGATCTGGAGAAATTTGTATCTGGACACCCCTCATTTATAGAGGC 836
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601 AGGTATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
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837 AGGTATACCATGATCGGAGTCCAAAGTGGACCTGGACAGGCTCAATGATGATCTCAAG 896
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661 CATTACAGTTGACCTCCCAAGGAATTAATCGGTCAATAAAGAGAGAGCTGAAGTTGGCC 720
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897 CGTTACAGTTGACCTCCCAAGGAATTAATCGGTCAATAAAGAGAGAGCTGAAGTTGGCC 956
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721 AATGTGCTCTTCTTCCAGTTGCTCTCGTGGAGAGCTGTTGGAGAAATGTTGGCTGT 780
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957 AATGAGCTCTTCTTCCAGTTGCTCTCGTGGAGAGCTGTTGGAGAAATGTTGGCTGT 1016
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781 GGAACTGTCAACTGGAGTTCCTGCACATGCAATTCAGGGAACCTGGAAGAAATGATCAT 840
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1017 GGAACTGTCAACTGGAGTTCCTGCACATGCAATTCAGGGAACCTGGAAGAAATGATCAT 1076
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901 CTAGTTGACATCCAGTTGGATCACCATGAACGATGCTGATGATCTGCAGCTCAAGACCA 960
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961 CTTGATATGAGAAATGTCACATCTCTTCAATTAAGCTGGAAGAACCTTTAGTTTAAAG 1020
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1286 ATGAATGCAATAGG-----AAATGTTGCTTTGTTAGTGCATGGCAAGAGAG 1334
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1141 GGTATATCATCACTTCTATACCTAAGATATAGGATGTCATTTAATATAGTGTGGAG 1200
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1335 CAAATATCATTAATTTCTATATACATAAATAGGAATTCATTTATCAATATGTTGAA 1394
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1201 GTTATATATGCAACACACACAGAAATATATGCTATGCTATGATATAGATCAAT 1260
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1395 GATATGATATATATATATATATACATGACTAGCTCTATG-----TATGTAATATAGATTAAT 1450
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1261 GTTTTCTTTTGGTATATATA 1279
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1451 ACTTTATTCAGTATATTA 1469
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RESULT 10

US-09-564-595D-52
; Sequence 52, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Mus musculus

; FEATURE:
; NAME/KEY: CDS
; LOCATION: (93)....(1205)
US-09-564-595D-52

Query Match 41.1%; Score 795.4; DB 4; Length 1472;
Best Local Similarity 78.7%; Pred. No. 5.1e-199;
Matches 1007; Conservative 0; Mismatches 226; Indels 46; Gaps 3;

QY 1 TTGTACCGAAGAGATGAGACCATCCAGTGAAGAAACGGCTAGCTCAGAGTCTCTAGA 60
DB |||||
QY 237 TTGTACCGAAGAGATGAGACCATCCAGTGAAGAAACGGCTAGCTCAGAGTCTCTCGC 296
DB |||||
QY 61 TTCCCGAAGACAGTACCCAGGAACTGCTCTCTGACATGCGCGCTTCACTCTCAGAGAA 120
DB |||||
QY 297 TTCCCGAAGACAGTACCCAGGAACTGCTCTCTGACATGCTGCTCCGTTCCAGGAGAA 356
DB |||||
QY 121 ACAGGATACAGTATGTTTGGACAATCAATGTTGGATAGAGGAGAGAAATGATATC 180
DB |||||
QY 357 ACAGGATACAACTGCTCTTTGACCATCAATTCGAGCTAGAGGAGAGAAATGACAT 416
DB |||||
QY 181 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACAGTACCATTTATAGAGA 240
DB |||||
QY 417 TGTAGGTATGATTTTGTGGAAGTTGAAGATCTCAGAGAGAGACACTGTTGTAGAGA 476
DB |||||
QY 241 CGATGTTGTGACACAGGAAAGTTCTCCAAAGGATAAATCAAGAAACGAAACCAATTTAA 300
DB |||||
QY 477 AGATGTTGTGCGCAAGAGAGATCCCTCCAAGGATAACGTCAAGAAACCAAGATTAA 536
DB |||||
QY 301 ATCATTCAAGTCCGATGACTACTTTGTGCTAAACCTGGATCAAGATTTATTTCT 360
DB |||||
QY 537 ATCATTCAAGTCCGATGACTACTTTGTGCTAAACCTGGATCAAGATTTATTTCT 596
DB |||||
QY 361 TTGTGGAAGATTTCCAAACCGCAGCAGCTTTCAGAGACCAACTGGGAATCTGTCAAGC 420
DB |||||
QY 597 TTGTGGAAGATTTCCAAACCGCAGCAGCTTTCAGAGACCAACTGGGAATCTGTCAAGC 656
DB |||||
QY 421 TCTATTTCCAGGGTATCTTAACTTCCATCAGTAAACCGATCCACACTGATGCGGAT 480
DB |||||
QY 657 TCTTTCTCTGGGGTCTCTTATCACTCTCATCAATAAGGACCCCACTCTCACTGCTGAT 716
DB |||||
QY 481 GCTCTGGAACAAATAATTTGACAGATTTGATACAGTGGAGATCTGCTCAAGTACTTCAAT 540
DB |||||
QY 717 GCTCTGGAACAAATAATTTGACAGATTTGATACAGTGGAGATCTTACTTAAGCACTTCAAT 776
DB |||||
QY 541 CCAGAGTCAATGGCAAGAGATCTTGAAGATATGATCTGGAACCCCTCGGTATCGAGC 600
DB |||||
QY 777 CCAGTCTTGGCAAGATGATCTGGAGATTTGATCTGGACACCCCTCATTTATAGAGC 836
DB |||||
QY 601 AGGTATACCATGACCGGAAGTCAAAAGTGAACCTGGATAGGCTCAATGATGCCAAG 660
DB |||||
QY 837 AGGTATACCATGATCGGAAGTCCAAAGTGGACCTGGACAGGCTCAATGATGATCTCAAG 896
DB |||||
QY 661 CGTTACAGTTGACCTCCCAAGGAATTAATCGGTCAATAAAGAGAGAGCTGAAGTTGGCC 720
DB |||||
QY 897 CGTTACAGTTGACCTCCCAAGGAATTAATCGGTCAATAAAGAGAGAGCTGAAGTTGGCC 956
DB |||||
QY 721 AATGTGCTCTTCTTCCAGTTGCTCTCGTGGAGAGCTGTTGGAGAAATGTTGGCTGT 780
DB |||||
QY 957 AATGAGCTCTTCTTCCAGTTGCTCTCGTGGAGAGCTGTTGGAGAAATGTTGGCTGT 1016
DB |||||
QY 781 GGAACTGTCAACTGGAGTTCCTGCACATGCAATTCAGGGAACCTGGAAGAAATGATCAT 840
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QY 1017 GGAACTGTCAACTGGAGTTCCTGCACATGCAATTCAGGGAACCTGGAAGAAATGATCAT 1076
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QY 841 GAGGTATTACAGTTGAGCTCGGCACATCAAGAGAGAGGCTGAAGAACCTATGGCT 900
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QY 901 CTAGTTGACATCCAGTTGGATCACCATGAACGATGCTGATGATCTGCAGCTCAAGACCA 960
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QY 1137 CTAGTTGACATCCAGTTGGATCACCATGAACGATGCTGATGATCTGCAGCTCAAGACCA 1196
DB |||||


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QY 961 CCTGATGAAGAAATGTCACATCTTACATTAAGCCCTGAAGAACCTTTAGTTAAGGA 1020
Db 1197 CCTGATAAAACACATGTCACATCTGTACTTTGATTATGAAGGACCTTTTAGGTTA 1252
QY 1021 GGGTGAGATAAGAGACCCCTTTTCTACAGCAACCAAACTTACTACTAGCCTGCAATGCA 1080
Db 1253 -----CAAACCCCTTAAGAGCTTCTAATCTCAGTGCA 1285
QY 1081 ATGAACACAAGTGTGCTGAGTCTCAGCCTTGCTTTGTTTAATGCCATGGAAGTAGAAA 1140
Db 1286 ATGAATGCATAGG-----AAATGTTGCTTTGTTAGTCCATGCGCAAGAAG 1334
QY 1141 GGTATATCATCACTTCTATACCTTAAGNATATAGATGGAATTAATATAGTGTGAG 1200
Db 1335 CAAATATCATTAATTTCTATATACATAACATAGGAATTCATTTATCAATAGTAGTGAA 1394
QY 1201 GTTATATATGACAAACACACACAGAAATATATTCATGCTATGTGTATATAGATCAAT 1260
Db 1395 GATATGTATATATCTTATATACATGACTAGCTCTATG-----TATGTAAATAGATTAAT 1450
QY 1261 GTTTTTTTGGTATATATA 1279
Db 1451 ACTTTATTCAGTATATTTA 1469

RESULT 11
US-09-808-972-3
; Sequence 3, Application US/09808972
; Patent No. 6630142
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 00-79
; CURRENT APPLICATION NUMBER: US/09/808,972
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/235,295
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/132,250
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (93)....(1205)
US-09-808-972-3

Query Match 41.1%; Score 795.4; DB 4; Length 1472;
Best Local Similarity 78.7%; Pred. No. 5.1e-199;
Matches 1007; Conservative 0; Mismatches 226; Indels 46; Gaps 3;

QY 1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAGAAACGGCTACGTGCAGAGTCCCTAGA 60
Db 237 TTGTACCGAAGAGAGAGAACATTCAGGTGACAGCAATGGCCATGTGCAGAGTCCCTGC 296
QY 61 TTCCCGAAGACAGTACCCAGGAACCTGCTCTGTGACATGCGCGCTTCACTCTCAGGAGAT 120
Db 297 TTCCCGAAGACAGTACCCAGGAACCTGCTCTGTGACATGCTGGCTCCGCTCCAGGAGAA 356
QY 121 ACACGGATACAGCTAGTGTGTTGACAAATCAGTTTGAATAGAGGAAGCAAAATGATATC 180
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Db 357 ACACGGATACAACTGTCTCTTTGACCATCAATTCGACTAGAGGAAGCAGAAAATGACATT 416
QY 181 TGTAAGTATGATTTTGTGGAAGTTGAAGATATATATCCGAAACCAAGTACCATTTATTAGAGGA 240
Db 417 TGTAAGTATGACTTTGTGGAAGTTGAAGAGTCTCAGAGAGCAGCAGCTGTTGTGAGAGGA 476
QY 241 CGATGTTGTCGACACAGGAAGTTCTTCCRAAGGATAAATCAAGAACGAAACCAATTTAAA 300
Db 477 AGATGTTGTGGCCCAAGAGGATCCCTCCAAGGATTAACGTCAAGAACCAACACAGATTAAA 536
QY 301 ATCATTCAAGTCCGATGATCTACTTTGTGCTAAACCTGGATTTCAAGATTTATTATTCT 360
Db 537 ATCATTTAAGTCTGATGATCTACTTTGTGCAAAACCTGGATTTCAAGATTTATTATTCA 596
QY 361 TTGCTGGAAGATTTTCAACCGCAGCAGCTTTCAGAGACCAACTGGGAATCTGTCACAAGC 420
Db 597 TTTGTGGAAGATTTTCAACCGGAGAGCCTTCAGAGACCAACTGGGAATCAGTCACAAGC 656
QY 421 TCTATTTTCAGGGGTATCCTATACTCTCCATCAGTAACGGATCCCACTCTGATTTCCGAT 480
Db 657 TCTTTCTCTGGGGTCTCTATCACTCTCCATCAATAACGGACCCCACTCTCACTGCTGAT 716
QY 481 GCTCTGGACAAAAAATTTGCAGAAATTTGATACAGTGGAAAGATCTGCTCAAGTACTTCAAT 540
Db 717 GCCCTGGACAAAATCTGCGAGAAATTCGATACCGTGGAGATCTACTTAAGCACTTCAAT 776
QY 541 CCAGAGTATGCGCAAGAGATCTTTGAGAATATGTATCTGGACACCCCTCGGTATGAGGC 600
Db 777 CCAGTGTCTTGGCAAGATGATCTGGAGAAATTTGTATCTGGACACCCCTCAATATAGAGGC 836
QY 601 AGTCTACCATGACCCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
Db 837 AGTCTACCATGATCGGAAGTCCAAAGTGGACCTGGACAGGCTCAATGATGATGTCAAG 896
QY 661 CGTTACAGTTGCACTCCCAAGAAATTTACTCGTCAATATATAGAGAGAGCTCAAGTTGCC 720
Db 897 CGTTACAGTTGCACTCCCAAGAAATTTACTCGTCAATATATAGAGAGAGCTCAAGTTGCC 956
QY 721 AATGTGTTCTTTTCCACGTTGCTCTCTCGTGCAGCGCTGTGGAGGAAATTTGGTGTGT 780
Db 957 AATGCACTTTCTTTCCACGATGCTCTCTCGTGCAGCGCTGTGGTGGCACTGTGTTGTC 1016
QY 781 GGAATCTCAATCGAGGTCTGCACATGCAATTCAGGAAAAACGTCGAAAAAGTATCAT 840
Db 1017 GGAATCTCAATCGAGGTCTGCACATGCAATTCAGGAAAAACGTCGAAAAAGTATCAT 1076
QY 841 GAGCTATTACAGTTTGAAGCTGGCCACATCAAGAGAGGGGTAGAGCTTAAGACCATGCT 900
Db 1077 GAGCTATTGAAGTTTGAAGCTGGCAATTTCAAGAGAGGGGCAAGCTTAAGAAATGCT 1136
QY 901 CTAGTTGACATCCAGTTGGATCACCAGAAAGATGCGATTTGATCTGAGCTCAAGACCA 960
Db 1137 CTGTTGATATCCAGCTGGATCATCATGAGCGATGTGACTGTATCTGCAGCTCAAGACCA 1196
QY 961 CCTCGATAAGAGAAATGTCACATCCTTTACATTAAGCTTGAAGAACCTTTAGTTTAAAGGA 1020
Db 1197 CCTCGATAAAACACATGTCACATCTGTACTTTGATTTATGAAGAGGACCTTTAGGTTA 1252
QY 1021 GGGTGAGATAAGAGACCCCTTTTCTACAGCAACCAAACTTACTACTAGCTGCAATGCA 1080
Db 1253 -----CAAACCCCTTAAGAGCTTCTAATCTCAGTGCA 1285
QY 1081 ATGAACACAAGTGTGCTGAGTCTCAGCCTTGCTTTGTTTAATGCCATGGAAGTAGAAA 1140
Db 1286 ATGAATGCATAGG-----AAATGTTGCTTTGTTAGTCCATGCGCAAGAAG 1334
QY 1141 GGTATATCATCACTTCTATACCTTAAGNATATAGATGGAATTAATATAGTGTGAG 1200
Db 1335 CAAATATCATTAATTTCTATATACATAACATAGGAATTCATTTATCAATAGTAGTGAA 1394
QY 1201 GTTATATATGACAAACACACACAGAAATATATTCATGCTCTATGTGTATATAGATCAAT 1260
Db 1395 GATATGTATATATCTTATATACATGACTAGCTCTATG-----TATGTAAATAGATTAAT 1450
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QY 1261 GTTTTGTGGTATATATA 1279
Db 1451 ACTTTATTCAGTATATTTA 1469

RESULT 12
US-09-564-595D-6
; Sequence 6, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: degenerate sequence
; NAME/KEY: misc_feature
; LOCATION: (1)...(1110)
; OTHER INFORMATION: n = A,T,C or G
US-09-564-595D-6

Query Match 36.1%; Score 697.6; DB 4; Length 1110;
Best Local Similarity 56.9%; Pred. No. 2,2e-173;
Matches 549; Conservative 259; Mismatches 157; Indels 0; Gaps 0;
QY 1 TTGTACCGAAGATGAGACCATCCAGGTGAAGAAACGGCTAGCTGAGAGTCTCTAGA 60
Db 145 YNTAYMGNGMGAYGARACNATHCARGTNAARGNAAAYGNGTAYGTNCCARWSNCCNMG 204
QY 61 TTCCGAAACAGCTACCCAGGACCTGCTCCGACATGCGGCTTCACCTCTCAGAGAAAT 120
Db 205 TTYCCNAAAYWSNTAYCCNMGNAAYTNTYTNACNTGGMGNTNCAIYWSNCARGARAY 264
QY 121 ACACGGATACAGTGTGTTGACATCAGTTTGGATTAGAGGAAGCAGAAATGATATC 180
Db 265 ACNMGNATHCARTYNTNTYGAAYCARTTYGNYTNGARGCNGCNGARAAYGAYATH 324
QY 181 TGAGGTATGATTTGTGGAAGTTGAAGATATATCCGAAACAGTACCATATTAGAGGA 240
Db 325 TGYMGNTAYGAYTTGTGNGARGTNGARGAYATHWSNGARACNWSNACNATHATHMGNGN 384
QY 241 CGATGTGTGGACACAGGAAGTTCTCCAGGATAAATCAAGACGAAACCAATATAA 300
Db 385 MGMTGTGTGGNCAIYARGHGTNCCNMGNATHAARWSNMGNAACNAYCARATHAAR 444
QY 301 ATCACATTTCAAGTCCGATGACTTTGTGGTAAACCTGGATTCAGATTTATTTCT 360
Db 445 ATHACNTTYAARWSNGAYGAYTAYTGTGNGCNAARCCNGNTTAAARATHAYTAYWSN 504
QY 361 TTGCTGGAAGATTTCCNACCCGAGAGCTTCAGACACCACTGCGAATCTGTCAAGC 420
Db 505 YTYNTNGARGAYTTYCARCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGC 564
QY 421 TCTATTTCAGGGGTATCTATACTCTCATCATAGTAACGATCCCACTCTGATGCGGAT 480
Db 565 WSNATHWSNGGNGTNSNTAYAYWSNCCNWSNGTACNGAYCCNACNNTYNATHGNCNGAY 624

QY 481 GCTCTGCACAAAAAATTGAGAAATTTGATACAGTGGAGAGATCTGTCAAGTACTTCAAT 540
Db 625 GCNYTNGAYAAARAATHGCGNGARTTYGACNGTNGARGAYTNTYTNAAARTAYTTTAA 684
QY 541 CCAGAGTCATGGCAAGAGATCTTGAGAAATATATCTGCGACACCCCTCGGTATCGAGGC 600
Db 685 CCNGARWSNTGGCARGAGAYTNGARAAATGATYTYNGAYACNCCMNGNTATMGNGN 744
QY 601 AGGTATACCATGACCGGAAGTCAAAAGTTGACCTGATAGGCTCAATGATGATGCCAAG 660
Db 745 MGWNSNTAYCAYGAYMGNAARWSNAARGTNGAYTYNGAYMGNTYNAAYGAYGAYGCAAR 804
QY 661 CGTTACAGTTGCACTCCAGGAATTACTCGGTCAATATAAGAGAGAGCTGAAGTTGCCC 720
Db 805 MGMTAYWSNTGYACNCCNMGNAAYTAYWSNGTNAAYATHMGNGARGARYTNAARYTNGCN 864
QY 721 AATGTGCTCTCTTCCACGTTGCTCTCGTCGAGCGCTGTGAGGAAATTTGGGCTGT 780
Db 865 AAYGTNGTNTTYYTCCMNGNTGYTNTYNTGTCNARMGNTGYGNGGNAAYTYGGNTGY 924
QY 781 GGAACTGTCAACTGGAGGTCTCTGCACATGCAATTCAGGGAAACCGTGAAAGATATCAT 840
Db 925 GGNACNGTNAAYTGMGNWSNTGYACNTGYAAYSNGNAAARACNCTNAARAARTAYCAY 984
QY 841 GAGGTATTACAGTTTGAGCCCTGGCCACATCAAGAGAGGGGTAGAGCTAAGACCATGCT 900
Db 985 GARGTNTYNCARTTYGARCNGGNCAYATHAARMGNGMNGMNGMNGNAAARACNATGCGN 1044
QY 901 CTAGTTGACATCCAGTTGGATCACCATGAAGATGCGGATCTGATCTGAGCTCAAGACCA 960
Db 1045 YTINGNGAYATHCARYTNGAYCAYCARGMNTGYGAYTYGATYHTGYWSNWSNMGCCN 1104
QY 961 CCTCG 965
Db 1105 CCNMG 1109
RESULT 13
US-09-438-046-3
; Sequence 3, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTIN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; CURRENT FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; EARLIER FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-438-046-3

Query Match 34.2%; Score 662; DB 4; Length 690;
Best Local Similarity 98.4%; Pred. No. 3.9e-164;
Matches 679; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 366 GGAAGATTTCACCCGAGAGCTTCAGAGACCACTGGGAATCTGTCAAGCTCTAT 425
DB 1 GGAAGATTTCACCCGAGAGCTTCAGAGACCACT-GGATCTGTCAAGCTCTGT 59
QY 426 TTCAGGGTATCTATAACTCTCCATCAGTAACCGATCCCACTCTGTGATGGGATGCTCT 485
DB 60 TTCAGGGTATCTATAACTCTCCATCAGTAACCGATCCCACTCTGTGATGGGATGCTCT 119
QY 486 GGACAAAAAATTGAGATTTGATACAGTGAAGATCTGCTCAAGTACTTCAATCCAGA 545
DB 120 GGACAAAAAATTGAGATTTGATACAGTGAAGATCTGCTCAAGTACTTCAATCCAGA 179
QY 546 GTCATGGCAAGAGATCTTGAGAAATATGATCTGCACACCCCTCGGTATCGAGGCGAGTC 605
DB 180 GTCATGGCAAGAGATCTTGAGAAATATGATCTGCACACCCCTCGGTATCGAGGCGAGTC 239
QY 606 ATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCAAGCGTTA 665
DB 240 ATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCAAGCGTTA 299
QY 666 CAGTTGCACTCCAGGAATTAATCGTCAATATAGAGAGAGCTGAAGTTGGCCAAATGT 725
DB 300 CAGTTGCACTCCAGGAATTAATCGTCAATATAGAGAGAGCTGAAGTTGGCCAAATGT 359
QY 726 GGTCTTTCTTCACAGTTGCTCTCGTCGAGCGCTGTGGAGAAATTTGGCTGTGGAAAC 785
DB 360 GGTCTTTCTTCACAGTTGCTCTCGTCGAGCGCTGTGGAGAAATTTGGCTGTGGAAAC 419
QY 786 TGTCAACTGGAGTCTTCACATGCAATTTCAAGGAAAAACCGTGAAAAAGTATCATGAGGT 845
DB 420 TGTCAACTGGAGTCTTCACATGCAATTTCAAGGAAAAACCGTGAAAAAGTATCATGAGGT 479
QY 846 ATTACAGTTGAGCTTGGCCATCAGAGAGGGGTAGAGCTTAAGACATGCTGTCTAGT 905
DB 480 ATTACAGTTGAGCTTGGCCATCAGAGAGGGGTAGAGCTTAAGACATGCTGTCTAGT 539
QY 906 TGACATCAGTTGGATCACCATGACGATGCGATTGTATCTGCAGCTCAAGACCACTCG 965
DB 540 TGACATCAGTTGGATCACCATGACGATGCGATTGTATCTGCAGCTCAAGACCACTCG 599
QY 966 ATAAGAGATGTGCATCTTACATTAAGCTGAAAGAACCTTTAGTTTAAAGGAGGTG 1025
DB 600 ATAAGAGATGTGCATCTTACATTAAGCTGAAAGAACCTTTAGTTTAAAGGAGGTG 659
QY 1026 AGATAAGAGACCTTTTCTTACCAGCAACC 1055
DB 660 AGATAAGAGACCTTTTCTTACCAGCAACC 689

RESULT 14
US-09-438-046-1
; Sequence 1, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: RASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
; FILE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; EARLIER FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10

; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; EARLIER FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-438-046-1

Query Match 18.4%; Score 355.2; DB 4; Length 360;
Best Local Similarity 99.2%; Pred. No. 1.1e-83;
Matches 357; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 769 AATTGTGCTCTGGAACCTGTCAACTGGAGGTCTTGACATGCAATTCAGGAAAAACCGTG 828
DB 1 AATTGTGCTCTGGAACCTGTCAACTGGAGGTCTTGACATGCAATTCAGGAAAAACCGTG 60
QY 829 AAAAAGTATCATGAGGTATTACAGTTTGAGCTGCGCCACATCAAGAGGAGGTAGAGCT 888
DB 61 AAAAAGTATCATGAGGTATTACAGTTTGAGCTGCGCCACATCAAGAGGAGGTAGAGCT 120
QY 889 AAGACCATGGCTCTAGTTGACATCCAGTTGATCACCATGACATGCGATGATGATCTGCG 948
DB 121 AAGACCATGGCTCTAGTTGACATCCAGTTGATCACCATGACATGATGATGATGATCTGCG 180
QY 949 AGCTCAAGACCACTTCGATAGAGAAATGTGACATCTCTTACATTAAGCTTGAAGAACCT 1008
DB 181 AGCTCAAGACCACTTCGATAGAGAAATGTGACATCTCTTACATTAAGCTTGAAGAACCA 240
QY 1009 TTAGTTTAAAGGAGGTGAGATAAGAGACCTTTTCTTACCAGCAACCACTTACTACTA 1068
DB 241 TTAGTTTAAAGGAGGTGAGATAAGAGACCTTTTCTTACCAGCAACCACTTACTACTA 300
QY 1069 GCCTGCAATGCAATGAACACAAAGTGGTTGCTGAGTCTCAGCTTCTGTTTAAAGCCAT 1128
DB 301 GCCTGCAATGCAATGAACACAAAGTGGTTGCTGAGTCTCAGCTTCTGTTTAAAGCCAT 360

RESULT 15
US-09-222-575-13/c
; Sequence 13, Application US/09222575
; Patent No. 6387697
; GENERAL INFORMATION:
; APPLICANT: Yuqiu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: Compositions for the Treatment and Diagnosis of Breast Cancer
; FILE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 210121.470
; CURRENT APPLICATION NUMBER: US/09/222,575
; CURRENT FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Human
US-09-222-575-13

Query Match 11.1%; Score 213.8; DB 3; Length 256;
Best Local Similarity 94.0%; Pred. No. 1.2e-46;
Matches 234; Conservative 0; Mismatches 12; Indels 3; Gaps 1;

QY 1423 TTGAATCTGCTCTCTTAAAGAAAGCATCTTGATATATAAAATCAAAAGATGAGGCTTT 1482

Db	256	TTGAATCTTGTCTTTTAAAGAACCATTTTGTATATTGAAATCAAAAGATGAGGCTTT	197
Qy	1483	CTTACATATACATCTTAGTTGATTATTAAGGAAAAA---GGTTCCAGAGAAAAGG	1539
Db	196	TTAACATATACATTTTAGTTGATTATTAAGGAAAAATATGTTTCCAGAGAAAAGG	137
Qy	1540	CCATACCTAGACATTTTCCATGAGAGCAGCTGACTGTAAT	1599
Db	136	CCATACCTAGACATTTTCCATGAGAGCAGCTGACTGTAAT	77
Qy	1600	AACTGTCTCCAAAACCATGCCATAATAATAAGTCTTTAGAAATTAATCATTTGTT	1659
Db	76	AACCTGTTTCCCAACCATGCCATAATAATAAGTCTTTAGAAATTAATCATTTGTT	17
Qy	1660	TTTTTATGC	1668
Db	16	TTTTTATGC	8

Search completed: October 31, 2004, 09:10:12
Job time : 190 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 04:51:22 ; Search time 5506 Seconds

(without alignments)
12799.572 Million cell updates/sec

Title: US-10-086-623-5

Perfect score: 1934

Sequence: 1 ttgtaccgaagagatgagac.....atcgactaaatggaacgcg 1934

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST.*

1: gb_est1.*

2: gb_est2.*

3: gb_hic.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_ges1.*

9: gb_ges2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1913.2	98.9	3739	3 AF113216	AF113216 Homo sapi
2	967.4	50.0	1095	9 AY419997	AY419997 Homo sapi
3	962.2	49.8	1095	9 AY419998	AY419998 Pan trogl
4	832.4	43.0	1797	3 AK003359	AK003359 Mus muscu
5	748.2	38.7	1095	9 AY419999	AY419999 Mus muscu
C 6	632.2	32.7	686	5 BU616629	BU616629 UI-H-DF0-
C 7	621.8	32.2	687	5 BU616664	BU616664 UI-H-DF0-
C 8	596.2	30.8	606	5 BQ575044	BQ575044 UI-H-EZ1-
C 9	524.6	27.1	580	5 BU685336	BU685336 UI-H-EZ1-
10	523.6	27.1	799	2 BE914552	BE914552 601665653
11	503.2	26.4	560	2 AW968905	AW968905 EST3803981
12	503.2	26.0	508	1 AL600063	AL600063 DKF2P313A
13	499.8	25.8	819	5 BU359805	BU359805 603477657
14	490.4	25.4	723	3 B1698994	B1698994 603477657
C 15	484.6	25.1	505	2 AW274723	AW274723 xn34b02.x
C 16	483.6	25.0	985	5 BU311960	BU311960 603405535
17	483.6	25.0	1044	5 BU213231	BU213231 603106994
C 18	482	24.9	485	1 AA488996	AA488996 aa54c10.s
19	477.2	24.7	727	5 BU326159	BU326159 603493350
20	473	24.5	480	5 BU431765	BU431765 UI-HF-BNO
21	455	23.5	798	5 BU404150	BU404150 603482511
22	434.4	22.5	969	6 CD242494	CD242494 AGENCOURT
C 23	428.4	22.2	554	7 CO603983	CO603983 DGB-274a2
24	423.8	21.9	811	5 BU326859	BU326859 603489249

C 25	420.4	21.7	551	7 CO596606	CO596606 DGB-130i1
C 26	413.8	21.4	467	4 BM144799	BM144799 TCAAP1D13
27	412.8	21.3	774	5 BU290871	BU290871 603607294
28	411.2	21.3	645	5 BU402438	BU402438 603483558
C 29	407.8	21.1	533	7 CO612657	CO612657 DGB-116n1
C 30	404.6	20.9	532	7 CO611691	CO611691 DGB-107b5
C 31	392	20.3	533	7 CO658472	CO658472 DGB-2023
C 32	387.2	20.0	921	5 BU315557	BU315557 603488052
C 33	386.8	20.0	406	1 AI221902	AI221902 G999h07.x
C 34	383	19.8	613	5 BU312449	BU312449 603544305
C 35	355.2	18.4	360	1 AA488780	AA488780 aa54c10.f
C 36	350.6	18.1	655	7 CO699403	CO699403 DGB-158p
C 37	345.6	17.9	455	7 CO600294	CO600294 DGB-1C24
C 38	335	17.0	761	7 CN078301	CN078301 EC2BBA14D
C 39	328.8	17.0	633	6 CF135616	CF135616 UI-HF-BNO
C 40	323	16.7	609	2 AW503454	AW503454 UI-HF-BNO
41	322	16.6	579	5 BU407817	BU407817 603483546
42	304	15.7	529	5 BU251898	BU251898 603404337
C 43	295.6	15.3	318	1 AA904948	AA904948 oJ81b10.s
C 44	293.4	15.2	317	1 AA736766	AA736766 oa23a03.s
45	292.8	15.1	762	5 BU384694	BU384694 603858418

ALIGNMENTS

RESULT 1
AF113216 3739 bp mRNA linear HTC 12-APR-2002

LOCUS AF113216 Homo sapiens MSTP036 mRNA, complete cds.

DEFINITION AF113216.1 GI:11640579

ACCESSION AF113216.1

VERSION HTC.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 3739)

AUTHORS Liu, B., Liu, Y.Q., Wang, X.Y., Zhao, X.Y., Sheng, H., Zhao, X.W., Liu, S., Xu, Y.Y., Ye, J., Song, L., Zhang, C.L., Zhang, J., Wei, Y.J., Cao, H.Q., Zhao, Y., Liu, L.S., Ding, J.F., Gao, R.L., Wu, Q.Y., Qiang, B.Q., Yuan, J.G., Liew, C.C., Zhao, M.S. and Hui, R.T.

TITLE Direct Submission

JOURNAL Submitted (15-DEC-1998) Molecular Medical Center for Cardiovascular Disease, Cardiovascular Institute, CAMS & PUMC, 167, Bei Li Shi Lu, Beijing 100037, P.R. China

FEATURES Location/Qualifiers

source 1..3739

organism="Homo sapiens"

mol_type="mRNA"

db_xref="taxon:9606"

tissue_type="aorta"

107..1219

codon_start=1

product="MSTP036"

protein_id="AAG39287.1"

db_xref="GI:11640580"

translation="MHRIFVYTLICANFCSDTSATPQASIKALRNANLRDRDES
HLTDYRDETIQVKGNGYVQSPFNSYPRNLLTWLHSDNTRIOLVFNQFGL
BAENDICRYDEVEDISETIIRGWCHEVPPRIKSTNOIKITFKSDDYFAK
PGKIIYSLLEDFOFAAASETWESVTSISGVSYNSFSDPTLIADALDKKIAEFD
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ORIGIN										
Query Match		98.9%		Score 1913.2		DB 3		Length 3739		
Best Local Similarity		99.7%		Pred. No. 0		Mismatches		3		
Matches 1928		Conservative		0		Indels		3		
Gaps								1		
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QY 61 TTCCGAAACAGTACCCAGGAACTGCTCTCTGACATGGCGCTTCACTCTCAGAGAAAT 120
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QY 1618 TGCCATATAATATAAGTGTCTTTAGAAATTAATCAATTTGCTTTTTTATGCAATTTGCTG 1677
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Db 1931 AGGATCCCTTATTTAAACACCTATCTCAAAACCTTACTTAGAAGCTTTTATGATTAATA 1990
QY 1738 GTCTTACAAAAGACAAATGTATAAGCTGTAAACAGAAATTTTGAATTTTCTTTGCAAAA 1797
Db 1991 GTCTTACAAAAGACAAATGTATAAGCTGTAAACAGAAATTTTGAATTTTCTTTGCAAAA 2050
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Db 2051 CCCCTCCACAAAAGCAAAATCCCTTCAAGAAATGGCAATGGGCAATCTGATGACCTTTTCCA 2110
QY 1858 GATGCTGTTCTAGTGAAGATGCTGGTACTGTGAGAACTTAAAGAGTGAACATTTGAACATC 1917
Db 2111 GATGCTGTTCTAGTGAAGATGCTGGTACTGTGAGAACTTAAAGAGTGAACATTTGAACATC 2170
QY 1918 GACGTAACCTGGAAA 1931
Db 2171 GACGTAACCTGGAAA 2184

RESULT 2
AY419997
LOCUS

DEFINITION

Homo sapiens HCM7077 gene, VIRTUAL TRANSCRIPT, partial sequence,

genomic survey sequence.

ACCESSION

AY419997

VERSION

AY419997.1

KEYWORDS

GSS.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

1095 bp DNA linear GSS 12-DEC-2003
Homo sapiens HCM7077 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
AY419997
AY419997.1 GI:39775954
GSS.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1095)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 1095)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence as made by sequencing genomic exons and ordering them
based on alignment.
FEATURES
source
1..1095
/organism="Homo sapiens"
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ORIGIN
Query Match 50.0%; Score 967.4; DB 9; Length 1095;
Best Local Similarity 99.9%; Pred. No. 7.5e-218;
Matches 968; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 TTGTACCGAAGAGATGAGACATCCAGGTGAAGGAACGGCTACGTGCAGAGCTCTAGA 60
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Qy 127 TTGTACCGAAGAGATGAGACATCCAGGTGAAGGAACGGCTACGTGCAGAGCTCTAGA 186
Db |||||||
Qy 61 TTCCGGAACAGCTACCCAGGAACTCTCTCGATGCGCGCTTCACTCTCAGGAGAAAT 120
Db |||||||
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Db |||||||
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Db |||||||
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Db |||||||
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Db |||||||
Qy 361 TTGCTGGAAGATTTCCAAACCGGACAGCTTCAGAGACCACTGGGATCTGCACAGC 420
Db |||||||
Qy 487 TTGCTGGAAGATTTCCAAACCGGACAGCTTCAGAGACCACTGGGATCTGTCCACAGC 546
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Db |||||||
Qy 601 AGGTATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGCTCTCAATGATGATGCCAAG 660
Db |||||||
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Db |||||||
Qy 847 AATGTGCTCTTTTCCACGTTGCTCTCTCGTGCAGCGCTGTGTGGAGAAATTTGGCTGT 906
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Qy 781 GGAACCTGCACTGAGAGGCTCTGACATGCAATTCAGGGAAACCGTGAAAAAGTATCAT 840
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Qy 961 CTTGATATA 969
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Qy 1087 CTTGATATA 1095
Db |||||||

RESULT 3
LOCUS AY419998 1095 bp DNA linear GSS 12-DEC-2003
DEFINITION Pan troglodytes HCM7077 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY419998
VERSION AY419998.1 GI:39775955
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE
1. (bases 1 to 1095)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 1095)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence as made by sequencing genomic exons and ordering them
based on alignment.
FEATURES
source
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/mol_type="genomic DNA"
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<1..>1095
/locus_tag="HCM7077"

ORIGIN
Query Match 49.8%; Score 962.2; DB 9; Length 1095;
Best Local Similarity 99.5%; Pred. No. 1.3e-216;
Matches 964; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 TTGTACCGAAGAGATGAGACATCCAGGTGAAGGAACGGCTACGTGCAGAGCTCTAGA 60
Db |||||||
Qy 127 TTGTACCGAAGAGATGAGACATCCAGGTGAAGGAACGGCTACGTGCAGAGCTCTAGA 186
Db |||||||
Qy 61 TTCCGGAACAGCTACCCAGGAACTCTCTCGTCAATATAGAGAAGAGCTGAAGTTGCC 120
Db |||||||

Db 187 TTCCCGAACAGCTACCCAGGAACTGCTCTCTGACATGCGCGCTTCACTCTCAGGAGAT 246
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Qy 241 CGATGGTGTGGACACAAGGAAGTTCTTCAAGGATAAATCAAGAACGACCAATTTAAA 300
Db 367 CGATGGTGTGGACACAAGGAAGTTCTTCAAGGATAAATCAAGAACGACCAATTTAAA 426
Qy 301 ATCACATTCAAGTCCGATGACTACTTGTGGCTAAACCTGGATTCAGGATTTATTATTCT 360
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Qy 421 TCTATTTCCAGGGATTCCTATTAATCTCTCATCAGTAAACGATCCCACTCTGATTCGGAT 480
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Qy 601 AGGTATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
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Db 1027 CTAGTTGACATCCAGTTGGATCACCATGACCATGATGATTTGATCTGCGAGCTCAAGACCA 1086
Qy 961 CCTCGATAA 969
Db 1087 CCTCGATAA 1095

RESULT 4

AK003359
LOCUS AK003359 1797 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:110003109 product:platelet-derived growth factor D mRNA, full insert sequence.
ACCESSION AK003359
VERSION AK003359.2 GI:26382601
KEYWORDS HTC; CAP trapper.

SOURCE ORGANISM

Mus musculus (house mouse)

Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS Carninci, P. and Hayashizaki, Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE

AUTHORS

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

11042159

REFERENCE

AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

20530913

11076861

REFERENCE

AUTHORS

The RIKEN Genome Exploration Research Group Phase II Team and the

FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

REFERENCE

AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 1797)

REFERENCE

AUTHORS

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,

Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,

Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,

Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M.,

Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M.,

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K.,

Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C.,

Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,

Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y.,

Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T.,

Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K.,

Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of

Physical and Chemical Research (RIKEN), Laboratory for Genome

Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,

URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,

Fax: 81-45-503-9216)

On Dec 10, 2002 this sequence version replaced gi:12833975.

Please visit our web site (<http://genome.gsc.riken.jp/>) for further

details.

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues. First strand cDNA was primed with a primer

[5'-GAGAGAGAGCGCGCACTCGAGTGTGTTTTTTTTTTT-3'], cDNA was

prepared by using trehalose thermo-activated reverse transcriptase


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genomic survey sequence.
ACCESSION AY419999
VERSION AY419999.1 GI:39775956
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence as made by sequencing genomic exons and ordering them
based on alignment.
FEATURES
source location/Qualifiers
1..1095
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1..>1095
/locus_tag="HCM7077"

gene
ORIGIN
Query Match 38.7%; Score 748.2; DB 9; Length 1095;
Best Local Similarity 85.8%; Pred. No. 5.7e-166;
Matches 831; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

QY 1 TTGTACCGAAGATGAGACCATCCAGGTGAAGGAACGGCTAGCTGCAGAGTCTCTAGA 60
DB 127 TTGTACCGAAGATGAGACCATCCAGGTGAAGGAACGGCTAGCTGCAGAGTCTCTGC 186
QY 61 TTCCCGAACAGCTACCCAGGACCTGCTCTGACATGGCGCTTCACTCTCAGAGAAAT 120
DB 187 TTCCCGAACAGCTACCCAGGACCTGCTCTGACATGGCGCTTCACTCTCAGAGAA 246
QY 121 ACACGGATACAGTGTGTTGACATCATGTTGGATTAGAGGAGCAGAAATGATATC 180
DB 247 ACACGGATACAGTGTGTTGACATCATGTTGGATTAGAGGAGCAGAAATGATATC 306
QY 181 TGTAGTATGTTTGTGAAGTTGAAGTATATCCGAAACAGTACCAATTATTAGAGGA 240
DB 307 TGTAGTATGTTTGTGAAGTTGAAGTATATCCGAAACAGTACCAATTATTAGAGGA 366
QY 241 CGATGTGTGGGACACAGGAAGTTCTCCCAAGTAAATCAAGAACCAACAAATTA 300
DB 367 AGATGTGTGGGACACAGGAAGTTCTCCCAAGTAAATCAAGAACCAACAAATTA 426
QY 301 ATCATTATCAAGTCCGATGACTACTTTGGTAAACCTGGATTCAAGATTATTATTC 360
DB 427 ATCATTATCAAGTCCGATGACTACTTTGGTAAACCTGGATTCAAGATTATTATTC 486
QY 361 TTGCTGGAAGATTTCACCGGAGCAGCTTCAGAGACCAACTGGGAATCTGTCAACG 420
DB 487 TTGCTGGAAGATTTCACCGGAGCAGCTTCAGAGACCAACTGGGAATCTGTCAACG 546
QY 421 TCTATTTCAGGGGTATCTTATTAATCTTCCATCAGTAAACCGATCCCACTCTGATGGGAT 480
DB 547 TCTTTCTCTGGGGTGTCTTATTAATCTTCCATCAGTAAACCGATCCCACTCTGATGGGAT 606
QY 481 GCTCTGGACAAAAAATTCAGAAATTTGATACAGTGGGAAGATCTGCTCAAGTACTTCAAT 540
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607 GCCCTGGACAAAACTGTCGAGAATTCGATACCGTGGGAAGATCTACTTTAAGCATTCAAT 666
541 CCAGAGTTCATGGCAAGAGATCTTGAAGATATGATCTGGACACCCCTCGGTATCGAGCC 600
667 CCAGTGTCTTGGCAAGATGATCTGGAGATTTGATCTGGACACCCCTCATTTAGAGCC 726
601 AGGTACATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
727 AGGTACATACCATGATCGGAAGTCCAAAGTGGACCTGGACAGGCTCAATGATGATCAAG 786
661 CGTTACAGTTCGATCCCGAGGAATTCCTGGTCAATATAGAGAGAGAGCTGAAGTTGCC 720
787 CGTTACAGTTCGATCCCGAGGAATTCCTGGTCAATATAGAGAGAGAGCTGAAGTTGCC 846
721 AATGTGTCTTCTTCCACAGTTGCTCTCTGAGGCTCTGAGGAGAAATTTGTGGTGT 780
847 AATGAGTCTTCTTCCACAGTTCCTCTCTGAGGCTCTGAGGAGAAATTTGTGGTGT 906
781 GGAATCTGCAACTGGAGTCTCTGACATGCAATTCAGGAGAAACCGTGAAGAAATGATCAT 840
907 GGAATCTGCAACTGGAGTCTCTGACATGCAATTCAGGAGAAACCGTGAAGAAATGATCAT 966
841 GAGGTATTACAGTTTGAGCTCTGACATGCAATTCAGGAGAAACCGTGAAGAAATGATCAT 900
967 GAGGTATTACAGTTTGAGCTCTGACATGCAATTCAGGAGAAACCGTGAAGAAATGATCAT 1026
901 CTAGTTGACATCCAGTTCGATCAGATGCAATTCAGGAGAAACCGTGAAGAAATGATCAT 960
1027 CTGTTGATATCCAGTTCGATCAGATGCAATTCAGGAGAAACCGTGAAGAAATGATCAT 1086
961 CCTCGATAA 969
1087 CCTCGATAA 1095

RESULT 6
BU616629/5
LOCUS BU616629
DEFINITION UI-H-DF0-ben-f-24-0-UI-s1 NCI CGAP DF0 Homo sapiens cDNA clone
UI-H-DF0-ben-f-24-0-UI 3', mRNA sequence.
ACCESSION BU616629
VERSION BU616629.1 GI:23282844
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 686)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 284-304, >AT rich#Low complexity (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.
location/Qualifiers
1..686
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cloned="UI-H-DF0-ben-f-24-0-UI"
/tissue_type="Subchondral Bone"
/dev_stage="Adult"
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/lab_host="DHI0B (Life Technologies)"
/clone_lib="NCI CGAP DF0"
/modified="Organ: Bone; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP DF0 is a cDNA library containing the following
tissue(s): Subchondral Bone. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT73-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GTTAAAGCGTC.
TAG LIB=UI-H-DF0
TAG_SEQ=GTAAAGCGTC"

ORIGIN
Query Match 32.7%; Score 632.2; DB 5; Length 686;
Best Local Similarity 98.7%; Pred. No. 1.5e-138;
Matches 660; Conservative 0; Mismatches 3; Indels 6; Gaps 2;

QY 1007 CTTTGTAGTTAAGGAGGTTGAGATAGAGACCCCTTTCTTACAGCAACAACTTACTAC 1066
DB |||||||
DB 686 CTTTGTAGTTAAGGAGGTTGAGATAGAGACCCCTTTCTTACAGCAACAACTTACTAC 627
QY 1067 TAGCCTGCAATGCAATGAACACAGTGGTGTGAGTCTCAGCCTTGCTTTGTTAATGCC 1126
DB |||||||
DB 626 TAGCCTGCAATGCAATGAACACAGTGGTGTGAGTCTCAGCCTTGCTTTGTTAATGCC 567
QY 1127 ATGCGAAGTAGAAGGTTATATCATCACTTCTATACCTAAGAAATATAGGATTGCAATTAA 1186
DB |||||||
DB 566 ATGCGAAGTAGAAGGTTATATCATCACTTCTATACCTAAGAAATATAGGATTGCAATTAA 507
QY 1187 TAATAGTGTGTTGAGTTATATATGACAAACACACACAGAAATATATTCATGCTATGTG 1246
DB |||||||
DB 506 TAATAGTGTGTTGAGTTATATATGACAAACACACACAGAAATATATTCATGCTATGTG 447
QY 1247 TATATAGTCAATG---TTTTTTTGTGTATATATACCGGTACACAGAGCTTACATA 1303
DB |||||||
DB 446 TATATAGTCAATGTTTTTTTTTGTGTATATATACCGGTACACAGAGGTTACATA 387
QY 1304 TGTTTGAGTTAGACTCTTAAATCTTTGCCAAAATAAGGGATGTCATAATATATGAAC 1363
DB |||||||
DB 386 TGTTTGAGTTAGACTCTTAAATCTTTGCCAAAATAAGGGATGTCATAATATATGAAC 327
QY 1364 ATGCTTTTAGAAAATTTAGGAGATAAATTTATTTTAAATTTTGAACACAAACAAATTT 1423
DB |||||||
DB 326 ATGCTCTTTAGAAAATTTAGGAGATAAATTTATTTTAAATTTTGAACACAAACAAATTT 267
QY 1424 TGAATCTTGCTCTCTTAAAGAAAGCATCTTGATATATTAATTAATTAATTAATTAATTAAT 1483
DB |||||||
DB 266 TGAATCTTGCTCTCTTAAAGAAAGCATCTTGATATATTAATTAATTAATTAATTAATTAAT 207
QY 1484 TTACATATACATCTTAGTTGATTATTAATAAGGAAAAA---GGTTTCCAGAGAAAGGC 1540
DB |||||||
DB 206 TTACATATACATCTTAGTTGATTATTAATAAGGAAAAATATGTTTCCAGAGAAAGGC 147
QY 1541 CAATACCTAAGCAATTTTTCATGAGAGCACTGCATACCTTACCTATGTTGGAAGCTGTAATA 1600
DB |||||||
DB 146 CAATACCTAAGCAATTTTTCATGAGAGCACTGCATACCTTACCTATGTTGGAAGCTGTAATA 87
QY 1601 ACCTGCTCCAAAACCATGCCATAATAATATATAGTGTCTTTAGAAATTAATTAATTTGTTT 1660
DB |||||||
DB 86 ACCTGCTCCAAAACCATGCCATAATAATATATAGTGTCTTTAGAAATTAATTAATTTGTTT 27
QY 1661 TTTTATGCA 1669
DB |||||||
DB 26 TTTTATGCA 18
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RESULT 7
BUG16664/c
LOCUS
DEFINITION
UI-H-DF0-ben-p-22-0-UI-s1 NCI CGAP DF0 Homo sapiens cDNA clone
UI-H-DF0-ben-p-22-0-UI 3', mRNA sequence.
ACCESSION
BUG16664
VERSION
BUG16664.1 GI:23282879
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 687)
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bentosoa@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 284-304, >AT rich#Low complexity (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.
Location/Qualifiers
1..687
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-DF0-ben-p-22-0-UI"
/tissue_type="Subchondral Bone"
/dev_stage="Adult"
/lab_host="DHI0B (Life Technologies)"
/clone_lib="NCI CGAP DF0"
/notes="Organ: Bone; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP DF0 is a cDNA library containing the following
tissue(s): Subchondral Bone. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT73-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GTTAAAGCGTC.
TAG LIB=UI-H-DF0
TAG_SEQ=GTAAAGCGTC"

ORIGIN
Query Match 32.2%; Score 621.8; DB 5; Length 687;
Best Local Similarity 98.5%; Pred. No. 4.2e-136;
Matches 660; Conservative 0; Mismatches 3; Indels 7; Gaps 3;

QY 1007 CTTTGTAGTTTAAAGGAGGTTGAGATAGAGACCCCTTTCTTACAGCAACAACTTACTAC 1066
DB |||||||
DB 687 CTTTGTAGTTTAAAGGAGGTTGAGATAGAGACCCCTTTCTTACAGCAACAACTTACTAC 628
QY 1067 TAGCCTGCAATGCAATGAACAC-AAGTGGTGTGCTGAGTCTCAGCCTTGCTTTGTTAATGC 1125
DB |||||||
DB 627 TAGCCTGCAATGCAATGAACACAAAGTGGTGTGCTGAGTCTCAGCCTTGCTTTGTTAATGC 568
QY 1126 CATGCGAAGTAGAAGGTTATATCATCACTTCTATACCTAAGAAATATAGGATTGATTTA 1185
DB |||||||
DB 567 CATGCGAAGTAGAAGGTTATATCATCACTTCTATACCTAAGAAATATAGGATTGATTTA 508
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QY 1186 ATAAATAGTGTGTTGAGGTTATATATGACAAAACACACACAGAAATATATTCATGTCTATGT 1245
D 507 ATAAATAGTGTGTTGAGGTTATATATGACAAAACACACACAGAAATATATTCATGTCTATGT 448
QY 1246 GTATATAGATCAAAATG---TTTTTTTGGTATATATAAACCAGGTACACAGAGCTTACAT 1302
D 447 GTATATAGATCAAAATGTTTGTGTTATATATAAACCAGGTACACAGAGGTACAT 388
QY 1303 ATGTTTGGCTAGACTCTTAAATCTTGGCCAAATAGGATGCTCAATATATGAAA 1362
D 387 ATGTTTGGCTAGACTCTTAAATCTTGGCCAAATAGGATGCTCAATATATGAAA 328
QY 1363 CATGTCTTTAGAAAATTTAGGAGATAAATTTATTTTAAATTTGAAACACAAAACAATT 1422
D 327 CATGTCTTTAGAAAATTTAGGAGATAAATTTATTTTAAATTTGAAACACAAAACAATT 268
QY 1423 TTGAATCTTGCTCTTAAAGAAAGCATCTTGTATATTAATAATCAAAAGATGAGGCTTT 1482
D 267 TTGAATCTTGCTCTTAAAGAAAGCATCTTGTATATTAATAATCAAAAGATGAGGCTTT 208
QY 1483 CTTACATATACATCTTGTGTTGATTATTAATAAGGAAAAA---GGTTTCCAGAGAAAAGG 1539
D 207 CTTACATATACATCTTGTGTTGATTATTAATAAGGAAAAAATATGTTTCCAGAGAAAAGG 148
QY 1540 CCAATACCTTAAGCATTTTTTCCATGAGAGCACTGCATATTTACCTATGTGACTGTAAAT 1599
D 147 CCAATACCTTAAGCATTTTTTCCATGAGAGCACTGCATATTTACCTATGTGACTGTAAAT 88
QY 1600 AACCTGTCTCCAAACCATGCCATATATATATAAGTCTTTTGAATTAATTAATCATTTGTT 1659
D 87 AACCTGTCTCCAAACCATGCCATATATATAAGTCTTTTGAATTAATTAATCATTTGTT 28
QY 1660 TTTTATATGCA 1669
D 27 TTTTATATGCA 18

RESULT 8
B0575044/c
LOCUS
DEFINITION
  UI-H-EZ1-bbd-o-15-0-UI.s1 NCI_CGAP_Ch2 Homo sapiens cDNA clone
  UI-H-EZ1-bbd-o-15-0-UI 3', mRNA sequence.
ACCESSION
  B0575044
VERSION
  B0575044.1 GI:21478361
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 606)
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.
  Email: cgaps-r@mail.nih.gov
  Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of
  Orthopaedics
  cDNA library preparation: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Cloning Distribution: Clone distribution information can be obtained
  from Dr. M. Bento Soares, bento-soares@uiowa.edu
  The following repetitive elements were found in this cDNA
  sequence: 1-24, xAT-rich#Low complexity 122-142,
  >AT-rich#Low complexity 249-325, >(TA)n#Simple_repeat
  Seq primer: M13 FORWARD
  POLYA=yes.
  Location/Qualifiers
    1..606
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
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/clone="UI-H-EZ1-bbd-o-15-0-UI"
/tissue_type="Chondrosarcoma Grade II"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_Ch2"
/note="Organ: Left Pelvis; Vector: pVT3-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI_CGAP_Ch2 is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma Grade II. The library
was constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dr primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pVT3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(ldr)18 tail. The sequence tag for this library is
TGATCACGCT.
TAG_TISSUE=grade-2-chondrosarcoma
TAG_LIB=UI-H-EZ1
TAG_SEQ=ATCTAATATG"
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ORIGIN

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Query Match      30.8%; Score 596.2; DB 5; Length 606;
Best Local Similarity 99.5%; Pred. No. 4.7e-130;
Matches 598; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 922 CACCATGAACGATGCGATTGTATCTGCAGCTCAAGACCACCTCGATAGAGAAATGTGCAC 981
D 606 CACCATGAACGATGCGATTGTATCTGCAGCTCAAGACCACCTCGATAGAGAAATGTGCAC 547
QY 982 ATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAAGAGGGTGAGATAAGAGACCCCTTT 1041
D 546 ATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAAGAGGGTGAGATAAGAGACCCCTTT 487
QY 1042 TCCTACCAAGCAACCAACTTACTACTAGCCTGCAATGCAATGAAACACAAAGTGGTGTCTGA 1101
D 486 TCCTACCAAGCAACCAACTTACTACTAGCCTGCAATGCAATGAAACACAAAGTGGTGTCTGA 427
QY 1102 GTCTCAGCCTTGTCTTTGTATGCAATGCCATGCCAGTAGTAAGGTATATCATCACTCTATA 1161
D 426 GTCTCAGCCTTGTCTTTGTATGCAATGCCATGCCAGTAGTAAGGTATATCATCACTCTATA 367
QY 1162 CCTAAGAATATAGGATTCGATTTAATAATAGTGTGAGGTTATATATATGCAACAAACACAC 1221
D 366 CCTAAGAATATAGGATTCGATTTAATAATAGTGTGAGGTTATATATATGCAACAAACACAC 307
QY 1222 ACAGAAATATATTCATGCTATGTGTATATAGATCAAAATGTTTTTTTGGTATATATAAC 1281
D 306 ACAGAAATATATTCATGCTATGTGTATATAGATCAAAATGTTTTTTTGGTATATATAAC 247
QY 1282 CAGGTACACCAAGCCTTACATATGTTTGGTGTAGACTCTTAAATCCTTTGCCAAATAAA 1341
D 246 CAGGTACACCAAGCCTTACATATGTTTGGTGTAGACTCTTAAATCCTTTGCCAAATAAA 187
QY 1342 GGGATGGTCAAAATATATGAAACATGCTCTTTAGAAAATTTAGGAGATAAATTTATTTTAA 1401
D 186 GGGATGGTCAAAATATATGAAACATGCTCTTTAGAAAATTTAGGAGATAAATTTATTTTAA 127
QY 1402 ATTTTGAACACAAACAAATTTTGAATCTTGTCTCTCTCTTAAAGAAAGCATCTTGTATATA 1461
D 126 ATTTTGAACACAAACAAATTTTGAATCTTGTCTCTCTCTTAAAGAAAGCATCTTGTATATA 67
QY 1462 AAAATCAAAAGATGAGGCTTCTTCTACATATACATCTTAGTTGATTTATTAAGAAAGAAA 1521
D 66 AAAATCAAAAGATGAGGCTTCTTCTACATATACATCTTAGTTGATTTATTAAGAAAGAAA 7

1522 A 1522
6 A 6
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RESULT 9
 BU685336 580 bp mRNA linear EST 07-OCT-2002
 LOCUS UI-CF-DUI-aav-f-05-0-UI.s2 UI-CF-DUI Homo sapiens cDNA clone
 DEFINITION UI-CF-DUI-aav-f-05-0-UI 3', mRNA sequence.
 ACCESSION BU685336
 VERSION BU685336.1 GI:23539180
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 580)
 REFERENCE Ronaldo, M.F., Lennon, G. and Soares, M.B.
 AUTHORS Normalization and subtraction: two approaches to facilitate gene
 TITLE discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PUBMED 889548
 COMMENT Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com) or from Open Biosystems
 (www.openbiosystems.com).
 The following repetitive elements were found in this cDNA
 sequence: 284-304, >ATrichLow_complexity (matched complement)
 Seq primer: M13 FORWARD
 PolIA-res.

FEATURES

Location/Qualifiers
 source
 1..580

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-CF-DUI-aav-f-05-0-UI"
 /tissue_type="Primary Lung Epithelial Cells"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-CF-DUI"
 /note="Organ: Lung; Vector: p773-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 UI-CF-DUI is a normalized cDNA library containing the
 following tissue(s): Primary Lung Epithelial Cells The
 library was constructed according to Bonaldo, Lennon and
 Soares, Genome Research, 6:791-806, 1996. First strand
 cDNA synthesis was primed with an oligo-dT primer
 containing a Not I site. Double stranded cDNA was ligated
 to an EcoR I adaptor, digested with Not I, and cloned
 directionally into p773-Pac vector. The oligonucleotide
 used to prime the synthesis of first-strand cDNA contains
 a library tag sequence that is located between the Not I
 site and the (dri)18 tail. The sequence tag for this
 library is GGCTGTAGGC.
 TAG TISSUE=Lung Epithelial Cells Tissue nos 359-368
 TAG LIB=UI-CF-DUI
 TAG_SEQ=GGCTGTAGGC"

ORIGIN

Query Match 27.1%; Score 524.6; DB 5; Length 580;
 Best Local Similarity 98.2%; Pred. No. 4.1e-113;
 Matches 553; Conservative 0; Mismatches 4; Indels 6; Gaps 2;
 QY 1113 GCTTTGTTAATGCCAGTAGAAGGTATATCATCACTTATACCTAGAAATAT 1172
 DB 580 GCTTTGTTAATGCCAGTAGAAGGTATATCATCACTTATACCTAGAAATAT 521

QY 1173 AGGATTGCATTATAATAGTGTGTTGAGTTTATATATGCAAAACACACACAGAAATATA 1232
 DB 520 AGGATTGCATTATAATAGTGTGTTGAGTTTATATATGCAAAACACACACAGAAATATA 461
 QY 1233 TTCAATGCTATGCTATATAGTCAATATG---TTTTTTTGGTATATATAACACGAGTACA 1289
 DB 460 TTCAATGCTATGCTATATAGTCAATATGTTTGTGTTATATATATATATATATATATAT 401
 QY 1290 CCAGAGCTTACATATGTTGAGTTAGACTCTTAAATCCTTTGGCAAAATAGGGATCGT 1349
 DB 400 CCAGAGCTTACATATGTTGAGTTAGACTCTTAAATCCTTTGGCAAAATAGGGATCGT 341
 QY 1350 CAATATATGAACATGCTTTAGAAAATTTAGAGATAAATTTATTTTAAATTTTGA 1409
 DB 340 CAATATATGAACATGCTTTAGAAAATTTAGAGATAAATTTATTTTAAATTTTGA 281
 QY 1410 ACACAAACAAATTTTGAATCTTCTCTCTTAAAGAAAGCATCTTGTATATTTAAATCA 1469
 DB 280 ACACAAACAAATTTTGAATCTTCTCTCTTAAAGAAAGCATCTTGTATATTTAAATCA 221
 QY 1470 AAGATGAGGCTTCTTACATATACATCTTGTATTTAAATAGGAAAAA---GGTT 1526
 DB 220 AAGATGAGGCTTCTTACATATACATCTTGTATTTAAATAGGAAAAAATATGTT 161
 QY 1527 TCCAGAGAAAGGCAATACCTAAGCATTTTTCATGAGAGCACTGCATACCTTACCTA 1586
 DB 160 TCCAGAGAAAGGCAATACCTAAGCATTTTTCATGAGAGCACTGCATACCTTACCTA 101
 QY 1587 TGTGCACTGTAATACCTGCTCTCAAAACCATGCAATATATATAGTGTCTTTAGAAAT 1646
 DB 100 TGTGCACTGTAATACCTGCTCTCAAAACCATGCAATATATATAGTGTCTTTAGAAAT 41
 QY 1647 TAAATCATTTGTGTTTTTTATGCA 1669
 DB 40 TAAATCATTTGTGTTTTTTATGCA 18

RESULT 10

BE914552
 LOCUS BE914552
 DEFINITION 60165653F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3965677 5',
 mRNA sequence.

ACCESSION BE914552
 VERSION BE914552.1 GI:10413295
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 799)
 REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM9137 row: j column: 14
 High quality sequence stop: 664.
 Location/Qualifiers
 1..799
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:3965677"
 /tissue_type="tumor, biopsy sample"

FEATURES

source
 Location/Qualifiers
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RESULT 12
AL600063          508 bp      mRNA      linear      EST 04-SEP-2003
LOCUS             DKFZp313A2132 r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
DEFINITION        DKFZp313A2132 5', mRNA sequence.
ACCESSION         AL600063
VERSION           AL600063.1 GI:15163351
KEYWORDS          EST.
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 508)
Bloecker,H., Boecher,M., Brandt,P., Mewes,W., Weil,B. and
Wiemann,S.
EST (Bloecker,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,B. and
Wiemann,S.)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone (DKFZp313A2132) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1..508
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp313A2132"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="313 (synonym: hlcc2)"
/note="Vector: pTriplex2; Site_1: Sf1A; Site_2: Sf1B;
cDNA-collection"

FEATURES
source
Query Match 26.0%; Score 503.2; DB 1; Length 508;
Best Local Similarity 99.4%; Pred. No. 4.6e-108;
Matches 505; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 162 GGAGCAGAAAATGATATCTGTAGGTATGATTTGTGGAAGTTGAAGATATATCGAAAC 221
DB 1 GGAAGCAAAAATGATATCTGTAGGTATGATTTGTGGAAGTTGAAGATATATCGAAAC 60

QY 222 CAGTACCAATTATTAGAGCAGCATGTGTGGACACAGGAAGTTCTCCCAAGGATAAATC 281
DB 61 CAGTACCAATTGTAGAGCAGCATGTGTGGACACAGGAAGTTCTCCCAAGGATAAATC 120

QY 282 AAGAACGACCAAAATTAATAATCACATTCAGTCCGATGACTACTTTGTGGTAAACCTGG 341
DB 121 AAGAACGACCAAAATTAATAATCACATTCAGTCCGATGACTACTTTGTGGTAAACCTGG 180

QY 342 ATTCAAGATTTATTATTTCTTTGCTGGAAGATTTCAACCCGAGCAGCTTCAGAGACCA 401
DB 181 ATTCAAGATTTATTATTTCTTTGCTGGAAGATTTCAACCCGAGCAGCTTCAGAGACCA 240

QY 402 CTGGGAATCTGCACAAGCTCTATTTTCAGGGGTATCTTAACTCTCCATCAGTAACCGA 461
DB 241 CTGGGAATCTGTCACTAGCTCTATTTTCAGGGGTATCTTAACTCTCCATCAGTAACCGA 300

QY 462 TCCCACTCTGATTGGGGATGCTCTGCACAAAAAATTCAGAAATTTGATACAGTGGGAAGA 521
DB 301 TCCCACTCTGATTGGGGATGCTCTGCACAAAAAATTCAGAAATTTGATACAGTGGGAAGA 360

QY 522 TCTGCTCAAGTACTTCAATCCAGAGTCTATGCGCAAGAAGATCTTTGAGAAATATGTATCTGGA 581
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DB 361 TCTGCTCAAGTACTTCAATCCAGAGTCTATGCGCAAGAAGATCTTTGAGAAATATGTATCTGGA 420
QY 582 CACCCCTCGGTATCGAGCAGGTATACCATGACCGGAAGTCAAAAGTTGACCTGGATAG 641
DB 421 CACCCCTCGGTATCGAGCAGGTATACCATGACCGGAAGTCAAAAGTTGACCTGGATAG 480
QY 642 GCTCAATGATATGCCAAGCGTTACAGT 669
DB 481 GCTCAATGATATGCCAAGCGTTACAGT 508

RESULT 13
BU359805          819 bp      mRNA      linear      EST 28-NOV-2002
LOCUS             603477657F1 CSEQHN71 Gallus gallus cDNA clone ChEST363b15 5', mRNA
DEFINITION        sequence.
ACCESSION         BU359805
VERSION           BU359805.1 GI:25867806
KEYWORDS          EST.
SOURCE            Gallus gallus (chicken)
ORGANISM          Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 819)
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
2235534
12445392
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1..819
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="ChEST363b15"
/dev_stage="36"
/lab_host="DH10B"
/clone_lib="CSEQHN71"
/note="Organ: hearts; Vector: pBluescript II KS(+);
Site 1: EcoRI; Site 2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand reaction, double-stranded cDNA
Following this first strand reaction, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bernaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

FEATURES
source
Query Match 25.8%; Score 499.8; DB 5; Length 819;
Best Local Similarity 79.6%; Pred. No. 3.3e-107;
Matches 617; Conservative 0; Mismatches 152; Indels 6; Gaps 2;

QY 91 CTGACATGGCGGCTCACTCTCAGAGAAATACAGGATACAGTAGTGTTCACATCAG 150
DB 1 CTGACATGGCGGCTCACTCTCAGAGAGACACAGGATCCAGCTGGCTTTTGTATTAATCAG 60

ORIGIN
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151 TTTGGATTAGAGGAGCAGAAAAATGATATCTGTAGGTATGATTTTGTGGAAGTTGAAGAT 210
Dbb |||||
61 TTTGGACTGGAGGAGCTGAAATGATATCTGCAGGTATGACTTTTGTGGAAGTTGAAGAT 120
Qy 211 ATATCCGAACCACTACCATTTATAGAGCAGATGTTGTGGACACAAAGGAAGTTCTCTCA 270
Dbb |||||
121 TTATCAGAGACCAAGCAGTATACAGGAAGGTGTGTGGGACAAAGGAAGTACCTCCA 180
Qy 271 AGGATAAAATCAAGAACCAACCAATTTAAATCACAATTCAGTCCGATGACACTACTTTGTG 330
Dbb |||||
181 AGAATTAACATCAAGAACCAATTCAGATAAGATTAACCTTCAATTCCTGACACTTTGTG 240
Qy 331 GCTAAACCTGGATTCAAGATTATTTATTTCTTGTCTGGAAGATTTCCAACCCGAGCAGCT 390
Dbb |||||
241 GCTAAACCAAGATTCAAGATTCTTACTCCCTTGTGGATGATTTCCAGC--ATGCAGCC 297
Qy 391 TCAGAGACCAACTGGGAATCTGTACAGCTCTATTTTCAGGGGTATCTCTATTAATCTCTCA 450
Dbb |||||
298 TCAGAAACCAACTGGGAATCAGTCAACAGCTCTGTCTCAGGGGTCTCTCTATCCCTCTCA 357
Qy 451 TCAGTAACGATCCCACTCTGATTGGGATGCTCTGCACAAAAAATTCGAGAAATTTGAT 510
Dbb |||||
358 TCAGTACCGACCTTACACTCAGCAGAGAGCCCTGGATCAGACCAATTTGCTGATTTGAC 417
Qy 511 ACAGTGGAAAGATCTGCTCAAGTACTTCAATCCAGAGTCTATGGCAAGAGATCTTGAGAT 570
Dbb |||||
418 ACTGTGGAAGATCTGCTTAAACACTTTAATCCAGACTCTCTGGAAAGAGATCTCGAAT 477
Qy 571 ATGTATCTGGACA--CCCTCGGTATCAGGAGGTCTATCATGACCGGAAGTCAAAA 627
Dbb |||||
478 TTGTACACAGAAAGTGGCCACCAATATTCAGGAGCAGGAGTACCATGACAGGAAGTCCAAA 537
Qy 628 GTTGACTCGATAGGCTCAATGATGATGCAAGCGTTTACAGTTGCACTCCAGGAATAC 687
Dbb |||||
538 GTTGACTCGACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 597
Qy 688 TCGTCAATATTAAGAGAGAGTGAAGTTGGCAATGTTGGTCTCTTTTCCAGTTGCCCTC 747
Dbb |||||
598 TCTGTCAATTAAGGGAAGAACTGAAGCTGACAAATGCTGTTTCTTCCCTCGCTGCCCTC 657
Qy 748 CTCGTGACGCGTGTGGAGAAATTTGGCTGTGGAAGTGTCACTGAGGAGTCTTCCGAC 807
Dbb |||||
658 CTGTGTCAGCGTGTGGAGAAATTTGGCTGTGGAAGTGTCAATTTGGGAAATCTCTGCAG 717
Qy 808 TCGAATTCAGGAAACCCGTGAAAAATATCATGAGGTATTACAGTTTGAGCGTG 862
Dbb |||||
718 TCGATGTCGGGAAACAGTGCACAAATATCATGAGGTGCTGCAAAATTTGTCCCG 772

RESULT 14
Bi689894
LOCUS 723 bp mRNA linear EST 18-SEP-2001
DEFINITION 60310727F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:534638 5',
mRNA sequence.
ACCESSION Bi689894
VERSION Bi689894.1 GI:15652523
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 723)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/ILLNL at:
<http://image.llnl.gov>
Plate: LLAM11880 row: f column: 07
High quality sequence stop: 692.
FEATURES
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/sex="female, virgin"
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/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam6"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

ORIGIN

Query Match 25.4%; Score 490.4; DB 4; Length 723;
Best Local Similarity 86.1%; Pred. No. 5.4e-105;
Matches 589; Conservative 0; Mismatches 91; Indels 4; Gaps 4;
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41 GGACTAGAGGAGCAGAAAAATGACATTTGTAGGTATGACTTTGTGGAAGTTGAAGAGTC 100
Qy 214 TCCGAAACCCAGTACCATTTATTAGAGG-ACGATGTTGTGGACACAAAGGAAGTTCTCTCAAG 272
Dbb |||||
101 TCAGAGAGCAGCAGCTGTTGTTCAGAGGACGATGTTGTGGCCACAAAGAGATCCCTCCAAG 160
Qy 273 GATTAATCAAGAGCAGAACCAATTAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 332
Dbb |||||
161 GATAACGTCAGAGAACCAACCCAGATTAATAATCAATCAATCAATCAATCAATCAATCAATCAAT 220
Qy 333 TAAACCTGGATTCAAGATTATTATTCTTCTCGAGAGATTCCAAACCCGAGCAGCTTC 392
Dbb |||||
221 AAACCTGGATTCAAGATTATTATTCTTCTCGAGAGATTTCAAACCCGAGCAGCTTC 280
Qy 393 AGAGACCAACTGGAAATCTGTCAAGCTCTATTTCAGGGGTATCTCTATAAATCTCTCCATC 452
Dbb |||||
281 AGAGACCAACTGGAAATCAGTCAAGCTCTTCTCTGGGGTGTCTATCACTCTCCATC 340
Qy 453 AGTAACGATCCCACTCTGATGGGATGCTCTGGACAAAAAATTCAGAAATTTGATAC 512
Dbb |||||
341 AATAACGAGACCCCACTCTCACTGCTGATGCCCTGGACAAAACTCTCGCAGAAATTCGATAC 400
Qy 513 AGTGAAGATCTGCTCAAGTACTTCAATCCAGAGTCTATGGCAAGAGATCTTGAGAAATAT 572
Dbb |||||
401 CGTGAAGATCTACTTAAGCACTTCAATCCAGTCTTCTTGGCAAGATGATCTGGAGAAATTT 460
Qy 573 GTATCTGGACACCCCTCGGTATCGAGCAGGTCTATCATGACCGGAAGTCAAAAGTTGA 632
Dbb |||||
461 GTATCTGGACACCCCTCATTTATAGAGCAGGTCTATCATGATCGGAAGTCAAAAGTTGA 520
Qy 633 -CCTGGATGCTCAATGATGATGCCAAGCGTTACGTTGCACTCCAGGAATTTACTCGG 691
Dbb |||||
521 CCCTGGACAGGCTCAATGATGATGATCAAGCGTTACGTTGCACTCCAGGAATTTACTCTG 580
Qy 692 TCAA-TATAAGAGAGAGCTGAAGTTGGCCCAATGGTCTTCTTTCCACCGTTGCTCTC 750
Dbb |||||
581 TGAACCTTCAGGAGAGAGCTGAAGTCAACATGCACTCTTCTTCCACAGATGCTCTCCTC 640
Qy 751 GTGACGCGCTGTGGAGGAAATTTGGCTGTGGAACTGTCAACTGTGAGAGGTCTGTGACATGC 810
Dbb |||||
641 GTGACGCGCTGTGGTGGCAACTGTGTGTGGGAACTGTC-ACTGGAAGTCTCTGCACATGC 699
Qy 811 AATTTCAGGAGAAACCGTGAAAGAG 834
Dbb |||||
700 AGCTCAGGAGACAGTGAAGAG 723


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RESULT 15
AW274723/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AW274723
xn34502.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695563 3',
mRNA sequence.
505 bp mRNA linear EST 03-JAN-2000

AW274723
AW274723.1 GI:6661753
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 505)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-f@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 475.
Location/Qualifiers
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/clone="IMAGE:2695563"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Kid11"
/notes="Organ: kidney; Vector: pTT73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(CloneIDs 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo."

```

ORIGIN	Query Match	25.1%;	Score 484.6;	DB 2;	Length 505;
	Best Local Similarity	98.8%;	Pred. No. 1.2e-103;		
	Matches 499;	Conservative 0;	Mismatches 4;	Indels 2;	Gaps 1;
Qy	1007	CTTTAGTCTTTAAGNGGCTGAGATAAGAGACCCCTTTTCTCTACCAGCACCAAACTTACTAC	1066		
Db	505	CTTTAGTCTTTAAGGAGGCTGAGATAAGAGACCCCTTTTCTCTACCAGCACCAAACTTACTAC	446		
Qy	1067	TAGCCTGCAATGCAATGAAACACAAAGTGGTTGCTGAGTCTCAGGCTTGCTTTGTTTAATGCC	1126		
Db	445	TAGCCTGCAATGCAATGAAACACAAAGTGGTTGCTGAGTCTCAGGCTTGCTTTGTTTAATGCC	386		
Qy	1127	ATGCCAAGTGAAGAGGTATATCATCAACTCTCTATACCTAGAAATATAGGATTCGATTAA	1186		
Db	385	ATGCCAAGTGAAGAGGTATATCATCAACTCTCTATACCTAGAAATATAGGATTCGATTAA	326		
Qy	1187	TAATAGTGGTTTGAGGTTATATATGCACAAACACACACAGAAATATATTCATGCTATGTG	1246		
Db	325	TAATAGTGGTTTGAGGTTATATATGCACAAACACACACAGAAATATATTCATGCTATGTG	266		
Qy	1247	TATATAGATCAAATGG--TTTCTTTTGGTATATATAACAGGTACACAGAGCTTACATAT	1304		

265	TATATAGATCAAAATGTTTTTTTTTTGGTATATATATACCAGGTACACACAGAGTTACATAT	206
Db		
1305	GTTTGAGTTAGACTCTTAAATCCTTTGCCAAATTAAGGGATGGTCAAAATATATGAAACA	1364
Qy		
205	GTTTGAGTTAGACTCTTAAATCCTTTGCCAAATTAAGGGATGGTCAAAATATATGAAACA	146
Db		
1365	TGTCCTTTAGAAAATTTAGGAGATAAATTTATTTTAAATTTTGNAAACACAAAACAATTTT	1424
Qy		
145	TGTCCTTTAGAAAATTTAGGAGATAAATTTATTTTAAATTTTGNAAACACAAAACAATTTT	86
Db		
1425	GAATCTTGCTCTCTTAAAGAAAGCATCTTCGTATATTAAAAATCAAAAGATGAGGCTTTCT	1484
Qy		
85	GAATCTTGCTCTCTTAAAGAAAGCATCTTCGTATATTAAAAATCAAAAGATGAGGCTTTCT	26
Db		
1485	TACATATACATCTTAGTTGAATATT	1509
Qy		
25	TACATATACATCTTAGATGAATTT	1
Db		

Search completed: October 31, 2004, 09:06:57
Job time : 5513 secs

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